Project Worksheet
fas ligand

Project Information

HGS Code	25750
Template ID	HTPAN08
Library	Human Pancreas Tumor
Project Name	fas ligand
Created By	Steve Ruben
Date Created	2/2/94

Nucleotide BLAST Analysis

Neucleotide Blast of HTPAN08 Full Contig + Screens

Query= HTPAN08XX   HGS #285507
        (1863 letters, both strands)

Database: nt
            162,249 sequences; 174,644,254 total letters.
Searching...done

Sequences producing High-scoring Segment Pairs:	High Score	Smallest Poisson Probability P(N)	N
gb|X55448|HSG6PDGEN Human complete G6PD gene for glucose-...	1029	2.9e-104	2
gb|K03021|HUMTPA Human tissue plasminogen activator (t...	830	2.0e-100	2
gb|M26434|HUMHPRTB Human hypoxanthine phosphoribosyltran...	830	4.6e-94	2
gb|T10601|T10601 hbc778 Homo sapiens cDNA clone hbc778...	1140	9.2e-87	1
gb|D00591|HUMRCC1 Human RCC1 gene, complete cds.	577	3.3e-85	3
gb|X69907|HSATPCP1 H.sapiens gene for mitochondrial ATP ...	618	2.3e-84	3
gb|M79078|M79078 EST01226 Homo sapiens cDNA clone HHCP...	1099	1.8e-83	1
gb|X68793|HSAT3 H.sapiens gene for antithrombin III	633	5.2e-83	2
gb|Z15027|HSHLA1467 H.sapiens HLA class III DNA	829	1.2e-82	2
gb|L10641|HUMVTDBP Human vitamin D-binding protein (GC) ...	721	1.4e-81	2

>gb\|X55448\|HSG6PDGEN Human complete G6PD gene for glucose-6-phosphate
    dehydrogenase >gb\|Z29527\|HSG6PHDH H.sapiens G6PD gene for
    glucose-6-phosphate dehydrogenase
    Length = 52,173

  Plus Strand HSPs:

  Score = 1029 (284.3 bits), Expect = 4.0e-75, P = 4.0e-75
  Identities = 245/294 (83%), Positives = 245/294 (83%), Strand = Plus

Query: 1570 TAAAAGATCGCAGTTTGCCTGGTGCAGTGGCTCACACCTGTAATCCCAACATTTTGGGAA 1629
              ||||| | | || || || ||||||||||||| |||||||||| || ||||||
Sbjct: 5032 TAAAATACAAAAATTGGCTGGGCGCAGTGGCTCACATCTGTAATCCCAGCACTTTGGGGG 5091

Ruben EXHIBIT #96

Project Information

HGS Code	25750
Template ID	HTPAN08
Library	Human Pancreas Tumor
Project Name	fas ligand
Created By	Steve Ruben
Date Created	2/2/94

Nucleotide BLAST Analysis

Nucleotide Blast of HTPAN08 Full Contig + Screens

Query= HTPAN08XX   HGS #285507
        (1863 letters, both strands)

Database: nt
          162,249 sequences; 174,644,254 total letters.
Searching..done

Sequences producing High-scoring Segment Pairs:	High Score	Smallest Poisson Probability P(N)	N
gb|X55448|HSG6PDGEN Human complete G6PD gene for glucose-...	1029	2.9e-104	2
gb|K03021|HUMTPA Human tissue plasminogen activator (t...	830	2.0e-100	2
gb|M26434|HUMHPRTB Human hypoxanthine phosphoribosyltran...	830	4.6e-94	2
gb|T10601|T10601 hbc778 Homo sapiens cDNA clone hbc778...	1140	9.2e-87	1
gb|D00591|HUMRCC1 Human RCC1 gene, complete cds.	577	3.3e-85	3
gb|X69907|HSATPCP1 H.sapiens gene for mitochondrial ATP ...	618	2.3e-84	3
gb|M79078|M79078 EST01226 Homo sapiens cDNA clone HHCP...	1099	1.8e-83	1
gb|X68793|HSAT3 H.sapiens gene for antithrombin III	633	5.2e-83	2
gb|Z15027|HSHLA1467 H.sapiens HLA class III DNA	829	1.2e-82	2
gb|L10641|HUMVTDBP Human vitamin D-binding protein (GC)	721	1.4e-81	2

>gb\|X55448\|HSG6PDGEN Human complete G6PD gene for glucose-6-phosphate
        dehydrogenase >gb\|Z29527\|HSG6PHDH H.sapiens G6PD gene for
        glucose-6-phosphate dehydrogenase
        Length = 52,173

   Plus Strand HSPs:

 Score = 1029 (284.3 bits), Expect = 4.0e-75, P = 4.0e-75
 Identities = 245/294 (83%), Positives = 245/294 (83%), Strand = Plus

Query: 1570. TAAAAGATCGCAGTTTGCCTGGTGCAGTGGCTCACACCTGTAATCCCAACATTTTGGGAA 1629
              ||||| | | || || || |||||||||||||| |||||||||| || ||||||
Sbjct: 5032 TAAAATACAAAAATTGGCTGGGCGCAGTGGCTCACATCTGTAATCCCAGCACTTTGGGGG 5091

Project Information

HGS Code	25750
Template ID	HTPAN08
Library	Human Pancreas Tumor
Project Name	fas ligand
Created By	Steve Ruben
Date Created	2/2/94

Nucleotide BLAST Analysis

Nucleotide Blast of HTPAN08 Full Contig + Screens

Query= HTPAN08XX   HGS #285507
        (1863 letters, both strands)

Database: nt
           162,249 sequences; 174,644,254 total letters.
Searching..done

Sequences producing High-scoring Segment Pairs:		High Score	Smallest Poisson Probability P(N)	N
gb|X55448|HSG6PDGEN	Human complete G6PD gene for glucose-...	1029	2.9e-104	2
gb|K03021|HUMTPA	Human tissue plasminogen activator (t...	830	2.0e-100	2
gb|M26434|HUMHPRTB	Human hypoxanthine phosphoribosyltran...	830	4.6e-94	2
gb|T10601|T10601	hbc778 Homo sapiens cDNA clone hbc778...	1140	9.2e-87	1
gb|D00591|HUMRCC1	Human RCC1 gene, complete cds.	577	3.3e-85	3
gb|X69907|HSATPCP1	H.sapiens gene for mitochondrial ATP ...	618	2.3e-84	3
gb|M79078|M79078	EST01226 Homo sapiens cDNA clone HHCP...	1099	1.8e-83	1
gb|X68793|HSAT3	H.sapiens gene for antithrombin III	633	5.2e-83	2
gb|Z15027|HSHLA1467	H.sapiens HLA class III DNA	829	1.2e-82	2
gb|L10641|HUMVTDBP	Human vitamin D-binding protein (GC) ...	721	1.4e-81	2

>gb|X55448|HSG6PDGEN Human complete G6PD gene for glucose-6-phosphate
       dehydrogenase >gb|Z29527|HSG6PHDH H.sapiens G6PD gene for
       glucose-6-phosphate dehydrogenase
       Length = 52,173

  Plus Strand HSPs:

  Score = 1029 (284.3 bits), Expect = 4.0e-75, P = 4.0e-75
  Identities = 245/294 (83%), Positives = 245/294 (83%), Strand = Plus

Query: 1570 TAAAAGATCGCAGTTTGCCTGGTGCAGTGGCTCACACCTGTAATCCCAACATTTTGGGAA 1629
              ||||| | . | || || || ||||||||||||||| ||||||||||| || |||||
Sbjct: 5032 TAAAATACAAAAATTGGCTGGGCGCAGTGGCTCACATCTGTAATCCCAGCACTTTGGGGG 5091

Project Information

HGS Code	25750
Template ID	HTPAN08
Library	Human Pancreas Tumor
Project Name	fas ligand
Created By	Steve Ruben
Date Created	2/2/94

Nucleotide BLAST Analysis

Neucleotide Blast of HTPAN08 Full Contig + Screens

Query= HTPAN08XX   HGS #285507
(1863 letters, both strands)

Database: nt
162,249 sequences; 174,644,254 total letters.
Searching..done

Sequences producing High-scoring Segment Pairs:		High Score	Smallest Poisson Probability P(N)	N
gb|X55448|HSG6PDGEN	Human complete G6PD gene for glucose-...	1029	2.9e-104	2
gb|K03021|HUMTPA	Human tissue plasminogen activator (t...	830	2.0e-100	2
gb|M26434|HUMHPRTB	Human hypoxanthine phosphoribosyltran...	830	4.6e-94	2
gb|T10601|T10601	hbc778 Homo sapiens cDNA clone hbc778...	1140	9.2e-87	1
gb|D00591|HUMRCC1	Human RCC1 gene, complete cds.	577	3.3e-85	3
gb|X69907|HSATPCP1	H.sapiens gene for mitochondrial ATP ...	618	2.3e-84	3
gb|M79078|M79078	EST01226 Homo sapiens cDNA clone HHCP...	1099	1.8e-83	1
gb|X68793|HSAT3	H.sapiens gene for antithrombin III	633	5.2e-83	2
gb|Z15027|HSHLA1467	H.sapiens HLA class III DNA	829	1.2e-82	2
gb|L10641|HUMVTDBP	Human vitamin D-binding protein (GC)	721	1.4e-81	2

>gb\|X55448\|HSG6PDGEN Human complete G6PD gene for glucose-6-phosphate
dehydrogenase >gb\|Z29527\|HSG6PHDH H.sapiens G6PD gene for
glucose-6-phosphate dehydrogenase
Length = 52,173

Plus Strand HSPs:

Score = 1029 (284.3 bits), Expect = 4.0e-75, P = 4.0e-75
Identities = 245/294 (83%), Positives = 245/294 (83%), Strand = Plus

```
Query:  1570 TAAAAGATCGCAGTTTGCCTGGTGCAGTGGCTCACACCTGTAATCCCAACATTTTGGGAA 1629
             |||||  | .   |  ||  ||  ||  |||||||||||||  ||||||||||  ||  | ||||||
Sbjct:  5032 TAAAATACAAAAATTGGCTGGGCGCAGTGGCTCACATCTGTAATCCCAGCACTTTGGGGG 5091
```

Project Information

HGS Code	25750
Template ID	HTPAN08
Library	Human Pancreas Tumor
Project Name	fas ligand
Created By	Steve Ruben
Date Created	2/2/94

Nucleotide BLAST Analysis

Neucleotide Blast of HTPAN08 Full Contig + Screens

Query= HTPAN08XX   HGS #285507
        (1863 letters, both strands)

Database: nt
          162,249 sequences; 174,644,254 total letters.
Searching...done

Sequences producing High-scoring Segment Pairs:		High Score	Smallest Poisson Probability P(N)	N
gb|X55448|HSG6PDGEN	Human complete G6PD gene for glucose-...	1029	2.9e-104	2
gb|K03021|HUMTPA	Human tissue plasminogen activator (t...	830	2.0e-100	2
gb|M26434|HUMHPRTB	Human hypoxanthine phosphoribosyltran...	830	4.6e-94	2
gb|T10601|T10601	hbc778 Homo sapiens cDNA clone hbc778...	1140	9.2e-87	1
gb|D00591|HUMRCC1	Human RCC1 gene, complete cds.	577	3.3e-85	3
gb|X69907|HSATPCP1	H.sapiens gene for mitochondrial ATP ...	618	2.3e-84	3
gb|M79078|M79078	EST01226 Homo sapiens cDNA clone HHCP...	1099	1.8e-83	1
gb|X68793|HSAT3	H.sapiens gene for antithrombin III	633	5.2e-83	2
gb|Z15027|HSHLA1467	H.sapiens HLA class III DNA	829	1.2e-82	2
gb|L10641|HUMVTDBP	Human vitamin D-binding protein (GC) ...	721	1.4e-81	2

>gb\|X55448\|HSG6PDGEN Human complete G6PD gene for glucose-6-phosphate
        dehydrogenase >gb\|Z29527\|HSG6PHDH H.sapiens G6PD gene for
        glucose-6-phosphate dehydrogenase
        Length = 52,173

  Plus Strand HSPs:

  Score = 1029 (284.3 bits), Expect = 4.0e-75, P = 4.0e-75
  Identities = 245/294 (83%), Positives = 245/294 (83%), Strand = Plus

Query: 1570 TAAAAGATCGCAGTTTGCCTGGTGCAGTGGCTCACACCTGTAATCCCAACATTTTGGGAA 1629
             ||||| | | || || || ||||||||||||| ||||||||||| || ||||||
Sbjct: 5032 TAAAATACAAAAATTCGCTGGGCGCAGTGGCTCACATCTGTAATCCCAGCACTTTGGGGG 5091

Project Information

HGS Code	25750
Template ID	HTPAN08
Library	Human Pancreas Tumor
Project Name	fas ligand
Created By	Steve Ruben
Date Created	2/2/94

Nucleotide BLAST Analysis

Nucleotide Blast of HTPAN08 Full Contig + Screens

Query= HTPAN08XX   HGS #285507
        (1863 letters, both strands)

Database: nt
          162,249 sequences; 174,644,254 total letters.
Searching...done

Sequences producing High-scoring Segment Pairs:	High Score	Smallest Poisson Probability P(N)	N
gb|X55448|HSG6PDGEN Human complete G6PD gene for glucose-...	1029	2.9e-104	2
gb|K03021|HUMTPA Human tissue plasminogen activator (t...	830	2.0e-100	2
gb|M26434|HUMHPRTB Human hypoxanthine phosphoribosyltran...	830	4.6e-94	2
gb|T10601|T10601 hbc778 Homo sapiens cDNA clone hbc778...	1140	9.2e-87	1
gb|D00591|HUMRCC1 Human RCC1 gene, complete cds.	577	3.3e-85	3
gb|X69907|HSATPCP1 H.sapiens gene for mitochondrial ATP ...	618	2.3e-84	3
gb|M79078|M79078 EST01226 Homo sapiens cDNA clone HHCP...	1099	1.8e-83	1
gb|X68793|HSAT3 H.sapiens gene for antithrombin III	633	5.2e-83	2
gb|Z15027|HSHLA1467 H.sapiens HLA class III DNA	829	1.2e-82	2
gb|L10641|HUMVTDBP Human vitamin D-binding protein (GC)	721	1.4e-81	2

>gb\|X55448\|HSG6PDGEN Human complete G6PD gene for glucose-6-phosphate
        dehydrogenase >gb\|Z29527\|HSG6PHDH H.sapiens G6PD gene for
        glucose-6-phosphate dehydrogenase
        Length = 52,173

  Plus Strand HSPs:

  Score = 1029 (284.3 bits), Expect = 4.0e-75, P = 4.0e-75
  Identities = 245/294 (83%), Positives = 245/294 (83%), Strand = Plus

Query: 1570 TAAAAGATCGCAGTTTGCCTGGTGCAGTGGCTCACACCTGTAATCCCAACATTTTGGGAA 1629
             ||||| |. | || || || ||||||||||||| |||||||||||| || ||||||
Sbjct: 5032 TAAAATACAAAAATTGGCTGGGCGCAGTGGCTCACATCTGTAATCCCAGCACTTTGGGGG 5091

```
Query:  1630 CCCAAGGTGGGTAGATCACGAGATCAAGAGATCAAGACCATAGTGACCAACATAGTGAAA 1689
             IIIIIIIIII IIIIIII II IIIIIIIIII IIIIII  II IIIIIII IIIIII
Sbjct:  5092 GCCAAGGTGGGCAGATCACAAGGTCAAGAGATCGAGACCATCCTGGCCAACATGGTGAAA 5151

Query:  1690 CCCCATCTCTACTGAAAGTGCAAAAATTAGCTGGGTGTGTTGGCACATGCCTGTAGTCCC 1749
             IIIIIIIIIIII III I IIIIIIIIIIIIIIII III III  I IIIIIIIIIIII
Sbjct:  5152 CCCCATCTCTACTAAAAATACAAAAATTAGCTGGGCGTGGTGGTGCGTGCCTGTAGTCCC 5211

Query:  1750 AGCTACTTGAGAGGCTGAGGCAGGAGAATCGTTTGAACCCGGGAGGCAGAGGTTGCAGTG 1809
             IIIIIII   IIIIIIIIIII IIIIIII IIIII I IIIII IIIIIIIIIIIIII
Sbjct:  5212 AGCTACTCAGTAGGCTGAGGCAGTAGAATCGCTTGAATCAGGGAGTCAGAGGTTGCAGTG 5271

Query:  1810 TGGTGAGATCATGCCACTACACTCCAGCCTGGGACAGAGCGAGACTTGGTTTC 1863
             I IIIIIII  IIIIII IIIIIIIIIIIIIIIIIIIIIIIIIIIIII II II
Sbjct:  5272 AGCTGAGATCGCGCCACTGCACTCCAGCCTGGGACAGAGCGAGACTCTGTCTC 5325

     Score = 133 (36.8 bits), Expect = 1.9, P = 0.85
     Identities = 53/86 (61%), Positives = 53/86 (61%), Strand = Plus

Query:  1569 CTAAAAGATCGCAGTTTGCCTGGTGCAGTGGCTCACACCTGTAATCCCAACATTTTGGGA 1628
             II IIII I     I II III II I IIII  I I IIIIIIIIIIII I   IIIIII
Sbjct: 34625 CTCAAAAAAAAAAAATTAGCCAGGCACGGTGGTGCGCGCCTGTAATCCCAGCTACTTGGGA 34684

Query:  1629 ACCCAAGGTGGGTAGATCACGAGATC 1654
             I III II   III I  II I
Sbjct: 34685 GGCTGAGGCAGGAGAATCGCTTGAAC 34710

     Score = 126 (34.8 bits), Expect = 0.0019, Poisson P(2) = 0.0019
     Identities = 50/81 (61%), Positives = 50/81 (61%), Strand = Plus

Query:  1568 ACTAAAAGATCGCAGTTTGCCTGGTGCAGTGGCTCACACCTGTAATCCCAACATTTTGGG 1627
             II IIII I     I I II II I   III II IIIIIIIIIIII I  IIIIII
Sbjct:    53 ACAAAAAAAAAAAAAAAATAGCTGGGAGTGATGGTGCATGCCTGTAATCCCAGCTATTTGGG 112

Query:  1628 AACCCAAGGTGGGTAGATCAC 1648
             II I III II  III I
Sbjct:   113 AAGCTGAGGCAGGAGAATCGC 133

  Minus Strand HSPs:

     Score = 888 (245.4 bits), Expect = 2.3e-63, P = 2.3e-63
     Identities = 220/273 (80%), Positives = 220/273 (80%), Strand = Minus

Query:  1854 TCTCGCTCTGTCGCCAGGCTGGAGTGTAGTGGCATGATCTCACCACACTGCAACCTCTGC 1795
             I IIIII  I  I I  II II IIIIII IIIIII IIIIIIII   IIIIIIIIIII I
Sbjct: 21011 TTTCGCCAGGCTGGCGTGCAGGAGTGCAGTGGCGTGATCTCAGTTCACTGCAACCTCCAC 21070

Query:  1794 CTCCCGGGTTCAAACGATTCTCCTGCCTCAGCCTCTCAAGTAGCTGGGACTACAGGCATG 1735
             I II III IIII  IIIIIIIIIIIIIIIIIIIII IIIIIIIIIIIIIIIIIIIIIIII
Sbjct: 21071 CACCTGGGGTCAAGTGATTCTCCTGCCTCAGCCTCCCAAGTAGCTGGGACTACAGGCACC 21130
```

6

```
Query:   1734 TGCCAACACACCCAGCTAATTTTTGCACTTTCAGTAGAGATGGGGTTTCACTATGTTGGT 1675
              ||||  ||||||  ||||||||||||||  |  |||  ||||||||||||||||||||  |||||||||
Sbjct:  21131 CGCCAGCACACACAGCTAATTTTTGTATTTTTAGTAGAGATGGGGTTTCACCATGTTGGT 21190

Query:   1674 CACTATGGTCTTGATCTCTTGATCTCGTGATCTACCCACCTTGGGTTCCCAAAATGTTGG 1615
              ||  |||||||  ||||||||||  |  ||||||||  |||||.|||  ||  |||  ||||  ||  |||
Sbjct:  21191 CAGGATGGTCTCTATCTCTTGACCCCGTGATCCACCCGCCTAGGCTTCTCAAAGTGCTGG 21250

Query:   1614 GATTACAGGTGTGAGCCACTGCACCAGGCAAAC 1582
              |||||||||    |||||||  ||||||  ||  ||
Sbjct:  21251 GATTACAGGCAAGAGCCACCCGCACCCAGCCCAC 21283


 Score = 878 (242.6 bits), Expect = 1.5e-62, P = 1.5e-62
 Identities = 218/271 (80%), Positives = 218/271 (80%), Strand = Minus

Query:   1856 AGTCTCGCTCTGTCGCCAGGCTGGAGTGTAGTGGCATGATCTCACCACACTGCAACCTCT 1797
              ||||||  ||||||||||||||||||||||||||||  |||||||||  ||||||  |  |  |||||||||||
Sbjct:  35428 AGTCTCACTCTGTCGCCAGGCTGGAGTGCAGTGGCATGGTCTCAGCTAACTGCAACCTCC 35487

Query:   1796 GCCTCCCGGGTTCAAACGATTCTCCTGCCTCAGCCTCTCAAGTAGCTGGGACTACAGGCA 1737
              |||  |||  |||||||||  ||||||||||||  ||||||||     |||||||||||  ||||||
Sbjct:  35488 GCCACCCAGGTTCAACTGATTCTCCTGCTTCAGCCTCCTGAGTAGCTGGGATTACAGGTG 35547

Query:   1736 TGTGCCAACACACCCAGCTAATTTTTGCACTTTCAGTAGAGATGGGGTTTCACTATGTTG 1677
              |  |||||  ||   |||  ||||||||||  |  ||||  ||||||     |||||||||  ||  ||
Sbjct:  35548 CGCGCCACCATGCCCCGGCTAATTTTTGTATTTTCTGTAGAGGCAGGGTTTCACCATCTTT 35607

Query:   1676 GTCACTATGGTCTTGATCTCTTGATCTCGTGATCTACCCACCTTGGGTTCCCAAAATGTT 1617
               ||||     |||||| ||  | | |||  |||  |||||||||||| |||  ||  |||  ||| |  |
Sbjct:  35608 GTCAGGCTGGTCTCGAACACCTGACCTCATGATCTACCCGCCTCGGCCTCCTAAAGTTCT 35667

Query:   1616 GGGATTACAGGTGTGAGCCACTGCACCAGGC 1586
              |||||||||||| ||||||||||||| || |||
Sbjct:  35668 GGGATTACAGGCGTGAGCCACTGCGCCCGGC 35698


 Score = 731 (202.0 bits), Expect = 2.9e-104, Poisson P(2) = 2.9e-104
 Identities = 191/247 (77%), Positives = 191/247 (77%), Strand = Minus

Query:   1863 GAAACCAAGTCTCGCTCTGTCGCCAGGCTGGAGTGTAGTGGCATGATCTCACCACACTGC 1804
              ||  ||  ||||||  |         |||||||  |||||  |||||||  |||||  |  ||||||
Sbjct:  24275 GAGACAGAGTCTTGTCTGTCACCCAGGCTTGAGTGCAGTGGCACAATCTCGGCTCACTGC 24334

Query:   1803 AACCTCTGCCTCCCGGGTTCAAACGATTCTCCTGCCTCAGCCTCTCAAGTAGCTGGGACT 1744
              |||||  | |||||| | || || |||||||||||||||||| |||||||||| | ||| |||||| |
Sbjct:  24335 AACCTTGGTCTCCCAGATTAAAGCGATTCTCCTCCCTCAGCCTCCCGAGTCACTGGGATT 24394

Query:   1743 ACAGGCATGTGCCAACACACCCAGCTAATTTTTGCACTTTCAGTAGAGATGGGGTTTCAC 1684
              |||||  ||  ||||||  |||  ||||||||||||||||  |  |||  |||||||||  |||||||||||
Sbjct:  24395 ACAGGTATATGCCACCACGCCCAGCTAATTTTTTTATTTTTAGTAGAGGTGGGGTTTCAC 24454
```

7

```
Query:  1683 TATGTTGGTCACTATGGTCTTGATCTCTTGATCTCGTGATCTACCCACCTTGGGTTCCCA 1624
             |||  |||||  ||  |  |||||||  ||  |||  |||  |||||||||  |||||||  ||   |||||
Sbjct: 24455 TATATTGGCCAGTCTGGTCTCGAACTCCTGACCTCGTGATCGCCCACCTCGGCCTCCCA 24514


Query:  1623 AAATGTT 1617
                ||  ||  |
Sbjct: 24515 AAGTGCT 24521
```

Protein BLAST Analysis

Protein Blast of HTPAN08 Full Contig + Screen

Query= HTPAN08XX   HGS#285507
         (1863 letters)

Translating both strands of query sequence in all 6 reading frames

Database: nr
           113,553 sequences; 31,868,292 total letters.
Searching...done

Sequences producing High-scoring Segment Pairs:		Reading Frame	High Score	Smallest Poisson Probability P(N)	N
pir|S|A40201	artifact-warning sequence (trans...	+3	241	1.4e-76	3
pir|S|C40201	artifact-warning sequence (trans...	+2	246	7.9e-59	2
pir|S|F40201	artifact-warning sequence (trans...	+3	180	1.1e-20	2
gp|X55777|HSMHCHHS_2	H.sapiens Mahlavu hepatocellular...	+3	190	1.9e-19	1
pir|S|D40201	artifact-warning sequence (trans...	+3	81	2.3e-18	4
gp|L27065|HUMNF2A_1	NF2 gene product [Homo sapiens]	-3	139	7.4e-14	1
gp|L20321|HUMSTK2A_1	protein serine/threonine kinase ...	-1	137	3.0e-12	1
pir|S|E40201	artifact-warning sequence (trans...	+2	98	1.0e-11	3
gp|S58722|S58722_1	X-linked retinopathy protein (3'...	-1	128	1.5e-11	1
pir|S|A46010	X-linked retinopathy protein (C-...	-1	128	1.5e-11	1
gp|M84237|HUMIGTB1A_2	integrin beta-1 subunit [Homo sa...	-3	116	1.9e-10	1
pir|S|A42442	beta 1 integrin subunit, beta 1S...	-3	116	1.9e-10	1
gp|L24521|HUMTRRP_1	transformation-related protein [...	-3	120	1.9e-09	1
gp|K02113|CHKVTTB_1	Chicken vitellogenin gene coding...	+3	72	1.0e-07	2

gp|L11672|HUMKRUPZN_1	zinc finger protein [Homo sapiens]	+1	108	1.9e-07	1
gp|X13607|GGVITIIG_1	vitellogenin [Gallus domesticus]...	+3	72	1.1e-06	2
gp|M18060|CHKVITC_1	Chicken vitellogenin gene, compl...	+3	72	1.1e-06	2
gp|U03470|RNU03470_1	ligand for Fas antigen [Rattus n...	+3	84	1.8e-06	2

>gp|U03470|RNU03470_1 ligand for Fas antigen [Rattus norvegicus]
       Length = 278

Plus Strand HSPs:

Score = 84 (40.9 bits), Expect = 0.0019, P = 0.0019
Identities = 15/34 (44%), Positives = 23/34 (67%), Frame = +3

```
Query:   750 GHSFLSNLHLRNGELVIHEKGFYYTYSQTYFRFQ 851
             G + +S +   + G LVI+E G Y++YS+ YFR Q
Sbjct:   164 GTALISGVKYKKGGLVINEAGLYFVYSKVYFRGQ 197
```

Score = 66 (32.2 bits), Expect = 1.8e-06, Poisson P(2) = 1.8e-06
Identities = 12/39 (30%), Positives = 22/39 (56%), Frame = +3

```
Query:   990 YSIYQGGIFELKENDRILVSVINEHLIDMDHEASFFGAF 1106
             +S Y G +F L   D + V+++   LI+ +   +FFG +
Sbjct:   238 HSSYLGAVFNLTVADHLYVNISQLSLINFEESKTFFGLY 276
```

Full Length Information

Full length sequence of HTPAN08XX HGS# 285507

```
GGCACGAGCACATTGTCTTCTCCAAACTCCAAGAATGAAAAGGCTCTGGGCCGCAAAATAAACTCCTGGGAATCATCAAGGAGTG
GGCATTCATTCCTGAGCAACTTGCACTTGAGGAATGGTGAACTGGTCATCCATGAAAAAGGGTTTTACTACATCTATTCCCAAAC
ATACTTTCGATTTCAGGAGGAAATAAAAGAAAACACAAAGAACGACAAACAAATGGTCCAATATATTTACAAATACACAAGTTAT
CCTGACCCTATATTGTTGATGAAAAGTGCTAGAAATAGTTGTTGGTCTAAAGATGCAGAATATCGACTCTATTCCATCTATCAAG
GGGGAATATTTGAGCTTAAGGAAAATGACAGAATTTGTGGTTTCTGTAACAAATGAGCACTTGATAGACATGGACCATGAAGCCA
GTTTTTTCGGGGCCTTTTTAGTTGGCTAACTGACCTGGAAAGAAAAAGCAATAACCTCAAAGTGACTATTCAGTTTTCAGGATGA
TACACTATGAAGATGTTTCAAAAAATCTGACCAAAACAAACAAACAGAAAACAGAAAACAAAAAACCCTCTATGCAATCTGAGTA
GAGCAGCCACAACCAAAAAATTCTACAACACACACTGTTCTGAAAGTGACTCACTTATCCCAAGAAAATGAAATTGCTGAAAGAT
CTTTCAGGACTCTACCTCATATCAGTTTGCTAGCAGAAATCTAGAAGACTGTCAGCTTCCAAACATTAATGCAATGGTTACATCT
TCTGGCTTTATAATCTACTCCTTGTAAAGACTGTAGAAGAAAACGCAACAATCCATCTCTCAAGTAGTGTATCACAGTAGTAGCC
TCCAGGTTTCCTTAAGGGACAACATCCTTAAGTCAAAAGAGAGAAGAGGCACCACTAAAAGATCGCAGTTTGCCTGGTGCAGTGG
CTCACACCTGTAATCCCAACATTTTGGGAACCCAAGGTGGGTAGATCACGAGATCAAGAGATCAAGACCATAGTGACCAACATAG
TGAAACCCCATCTCTACTGAAAGTGCAAAAATTAGCTGGGTGTGTTGGCACATGCCTGTAGTCCCAGCTACTTGAGAGGCTGAGG
CAGGAGAATCGTTTGAACCCGGGAGGCAGAGGTTGCAGTGTGGTGAGATCATGCCACTACACTCCAGCCTGGCGACAGAGCGAGA
CTTGGTTTCAAAAAAAAAAA
```

HGS

Human Genome Sciences, Inc.
Matched Sequence Worksheet
HTPAN08R   : tumor necrosis factor (TNF-alpha)

Search Results

Description	:	Score	Overlap	Start	End	% Sim	% Iden	LEnd	REnd	Date	Meth
Tumor necrosis factor precursor - Human	:	20	PIR:A44189	104	143	57.50	35.00	59	178	08/24/93	zest
TUMOR NECROSIS FACTOR PRECURSOR (TNF-ALPHA) (CAG	.	20	SP:P01375	104	143	57.50	35.00	59	178	08/24/93	zest

Sequence

tumor necrosis factor (TNF-alpha)

HTPAN08R   Length: 230 Sunday 20, 1993 13:50 Check: 9601 ..

```
  1 CACATTGTCT TCTCCAAACT CCAGAATGA AAAGCCTCTG GGCGGCAAAA
 51 TAAACTCCTG CGAATCATCA AGGAGTGGGC ATTCATTCCT GAGCAACTTG
101 CACTTGAGGA ATGGTGAACT GGTCATCCAT GAAAAGGGT TTTACTTACAT
151 CTATTCCTAA ACATACTTTG GATTTCAGGA CCTTTATAAAA GAAAACACAA
201 AGAACGNCAA AGAAATGGTC CAATATATTT
```

                                                        44-5

                                                        1573

HGS Sequencing Worksheet

INVESTIGATOR: AK, Ho, Suk, LC, DB
LIBRARY/METHOD: Misc DP/DT?

DATE: 9/1
PLATE #: _____

Sample No.	Sample Name	Sample Preparation Comments	Chemistry Dye Prim/ Dye Term	Primer Name	Sequence Protocol	Sequence Comments	
1	HTPBC24Ra	AK boiling	DP	Reverse		NS	N
2	HTPBC24Rb					weak	R
3	HIBCW23Ra						320
4	HIBCW23Rb					NS-weak	BNS
5	HTPAN08Ra					miss-C	*
6	HTPAN08Rb	↓	↓			miss-C	R
7	HIBCK00R	Ho Magic Mini				weak	M
8	HPMAM00R	↓ ↓					282
9	HTEAH87R	Suk Midi					391
10	HPLEB38R					weak	NS
11	HIBEH64R	↓ ↓				weak	37 369
12	PGEM( )R	control			↓		370
13	HTPBC24Fa	AK boiling		Forward		NS-weak	ND
14	HTPBC24Fb						350
15	HIBCW23Fa						344
16	HIBCW23Fb					NS-weak	NDF
17	HTPAN08Fa						320
18	HTPAN08Fb	↓ ↓					405
19	HTEAH87F	Suk Midi				weak	M
20	HPLEB38F						276
21	HIBEH64F	↓ ↓					477
22	HIBCK00F	Ho Magic Mini					426
23	HPMAM00F	↓ ↓ ↓				weak poly T, DK	
24	HASSB35F	LC		↓		weak poly T	R
25	PGEM( )DT	control	DT				*
26	HIBCK000692	Ho		692		weak-NS	N
27	HPMAM000693	↓		693		weak-NS	M
28	HFKBE9500647	DB boiling		647			340
29	HIBEI0200646	↓ ↓		646		weak-NS	340
30	HASSB35000001	LC		VDRF1			293
31	HASSB3500187	↓		G187			R
32							
33							
34							
35							
36							

Additional Comments:

Date of Run: 9-10-73

Catalyst #: 8-10-93 Manual RYS/KPC

Sequencer #: 09
Results Folder: 9-1-13 DNA09

Blast Analysis: _____

Renee 12

HGS Sequencing Worksheet

Sample No.	Sample Name	Sample Preparation Comments	Chemistry Dye Prim/ Dye Term	Primer Name	Sequence Protocol	Sequence Comments	
1	HTPBC24Ra	AK boiling	DP	Reverse		NS	N
2	HTPBC24Rb					weak	R
3	HIBCW23Ra						320
4	HIBCW23Rb					NS-weak	NS
5	HTPANO8Ra					miss-C	*
6	HTPAN08Rb	↓	↓			miss-C	R
7	HIBCK00R	Ho Magic Mini				weak	M
8	HPMAM00R	↓	↓				282
9	HTEAH87R	Suk Midi					391
10	HPLEB38R					weak	NS
11	HIBEH64R	↓	↓			weak	57 369
12	PGEM( )R	control			↓		370
13	HTPBC24Fa	AK boiling		Forward		NS-weak	NS
14	HTPBC24Fb						350
15	HIBCW23Fa						344
16	HIBCW23Fb					NS-weak	NDF
17	HTPANO8Fa						320
18	HTPAN08Fb	↓	↓				405
19	HTEAH87F	Suk Midi				weak	M
20	HPLEB38F						276
21	HIBEH64F	↓	↓				477
22	HIBCK00F	Ho Magic Mini					426
23	HPMAM00F	↓ ↓ ↓				weak poly T, DK	
24	HASSB35F	LC			↓	weak poly T	R
25	PGEM( )DT	control	DT				*
26	HIBCK000624	Ho		692		weak NS	N
27	HPMAM000693	↓		693		weak-NS	M
28	HFKBE9500647	DB boiling		647			340
29	HIBEI0200646	↓ ↓		646		weak-NS	341
30	HASSB3500001	LC		VDRF1			293
31	HASSB3500187	↓		G187			R
32							
33							
34							
35							
36							

Additional Comments:

Date of Run: 9-10-73

Catalyst #: 9-10-73 Manual RVS/HHC

Sequencer #: 09

Results Folder: 9-1-73 DAA09

Blast Analysis: _____

Renee

13

HGS Sequencing Worksheet

INVESTIGATOR: JG, GLY, JW, AMK
LIBRARY/METHOD:

DATE: 9/14/03
PLATE #:

Sample No.	Sample Name	Sample Preparation Comments	Chemistry Dye Prim/ Dye Term	Primer Name	Sequence Protocol	Sequence Comments
1	HTFCU19Fa	JG. boiling	DP	Forward		T
2	HTFCU19Fb					MIT
3	HE88B07Fa					
4	HE88B07Fb	↓ ↓				weak
5	HLHAC23Fb	GLY boiling				
6	HFCAW19Fb	↓				N weak
7	ZFBR307F	JW Magic mini				N weak
8	PGEM(M13)F	control				
9	HTFCU19Ra	JG boiling		Reverse		
10	HTFCU19Rb					
11	HE88B07Ra					
12	HE88B07Rb	↓ ↓				
13	HPLIB74Rb	GLY boiling				
14	HPRAA08Rb	magic				weak
15	HPLB227Rb					weak
16	HPMAK36Rw					weak
17	KPMAK36Rb	↓ ↓				weak
18	ZFBR307R	JW Magic Mini				weak R
19	HTPAN08Ra	AMK				
20	HTPAN08Rb	↓				
21	PGEM(635)R	control	↓	↓		
22						
23						
24						
25						
26						
27						
28						
29						
30						
31						
32						
33						
34						
35						
36						

repeat 19, repeat 20

Reverse LOT A31/000R / Forward A3EC08B

Additional Comments:
Date of Run: 9/14/93
Catalyst #: Biomek mix + KAG
Sequencer #: 05
Results Folder: 09/15/93 DNA 05 KAG
Blast Analysis:

Kris G   14

HGS Sequen~ing Worksheet

INVESTIGATOR: JG, GLY, JW, AMK

LIBRARY/METHOD:

DATE: 9/14/93

PLATE #:

Sample No.	Sample Name	Sample Preparation Comments	Chemistry Dye Prim/ Dye Term	Primer Name	Sequence Protocol	Sequence Comments
1	HHFCU19Fa	JG, boiling	DP	Forward		T
2	HHFCU19Fb					HIT
3	HE8BB07Fa					
4	HE8BB07Fb	↓	↓			weak
5	HLHAC23Fb	GLY, boilig				
6	HFCAW19Fb	↓				N weak
7	ZFBR307F	JW Magic mini				N weak
8	PGEM(sis)F	control				
9	HHFCU19Ra	JG boilig		Reverse		
10	HHFCU19Rb					
11	HE8BB07Ra					
12	HE8BB07Rb	↓	↓			
13	HPLIB74Rb	GLY boilig				
14	HPRAA08Rb	magic				weak
15	HPLBQ27Rb					weak
16	HPMAK36Rw					weak
17	KPMAK36Rb	↓	↓			weak
18	ZFBR307R	JW Magic Mini				weak R
19	HTPAN08Ra	AMK				
20	HTPAN08Rb	↓				
21	PGEM(-35)R	Control	↓	↓		
22						
23						
24						
25						
26						
27						
28						
29						
30						
31						
32						
33						
34						
35						
36						

repeat (19), *repeat* (20)

dditional Comments:

Date of Run: 9/14/93   **Sequencer #:** 05

Catalyst #: Biomek mix + KAG **Results Folder:** 09/15/93 DNA 05 KAG

Blast Analysis: _____

RunS

15

```
HHFCUI9G    101,66,42,27 8S 12.32   Trash T    ·7 PolyT at 55
HHFCUI9Fb   93,94,66,39 8S 12.94    Trash M/T  PolyT at 53; appears mixed
HE8BB07Fa   114,55,42,43 8S-12.00   72→310   —  124/310-72
HE8B207Fb   67,78,43,27 4S-12.00    80→300     14N/300-30
HLHAC23Fb   29,71,50,43 73 11.76    105→290    3N/290-05
HFCAWI9Fb   no analyzed data  N
ZFBR307F    no analyzed data  N
PGEM025F    112,109,45,53 8S-12.00  104→285    7N/285-104
HHFCUI9Ra   123,95,73,60 3S 12.51   106→410⁺   2N/410-106
HHFCUI9Rb   112,82,55,59 8S 12.95   103→410⁺   2N/410-103
HE8BB07RG   172,15,29,09 8S 12.95   104→410⁺   1N/410-04
HE8B307Rb   246,137,105,88 8S 12.37 68→410⁺    2N/410-68
HPLYB74Rb   109,90,62,52 6S 12.51   104→440⁺   6N/440-104
HPRAAO8Rb   80,54,38,33 8S 13.36    87→420⁺    1CN/420-87
HPLBG27Rb   73,45,37,34 8S 13.48    55→310⁺    7N/310-55
HPMAK362w   no analyzed data  N
HPMAK362b   74,53,42,33 8S 13.03    87→430⁺    1CN/430-87
ZFBR307R    44,35,36,26 1S-12.00    Trash R
HTPANO8Rg   155,115,86,95 8S 12.82  105→420    8N/420-105
HTPANO8Rb   107,96,66,50 8S 12.13   52→420⁺    7N/420-52
PGEM038R    94,55,44,35 8S 13.25    37→310     14N/310-37
```

16

Human Genome Sciences, Inc.
Matched Sequence Worksheet
HTPAN08R : tumor necrosis factor (TNF-alpha)

Search Results

Description	Score	Overlap	Start	End	% Sim	% Iden	LEnd	REnd	Date	Meth
Tumor necrosis factor precursor - Human	20	PIR:A44189	104	143	57.50	35.00	59	178	08/24/93	zast
TUMOR NECROSIS FACTOR PRECURSOR (TNF-ALPHA) (CAC	20	SP:P01375	104	143	57.50	35.00	59	178	08/24/93	zast

Sequence

tumor necrosis factor (TNF-alpha)

HTPAN08R   Length: 230 Sunday 20, 1993 13:50 Check: 9601 ..

```
   1  CACATTGTCT TCTCCAAACT CCAAGAATGA AAAGGCTCTG GGCGCGAAAA
  51  TAAACTCCTG GGAATCATCA AGGAGTGGGC ATTGATTCCT GAGCAACTTG    46-5
 101  CACTTGAGGA ATGGTGAACT GGTCATCCAT GAAAAAGGGT TTTACTACAT
 151  CTATTCCCAA ACATTCCTTC GATTTCAGGA GGAAATAAAA GAAAACACAA    1575
 201  AGAACGCNCAA ACAAATGGTC CAATATATTT
```

Applied Biosystems

Synthesis Order - htpan08 157-s

Run date: 9/20/93
Run ID: 685 AMK
Customer: amk   _Zlemer_

1.   KH
2.
Synthesizer: Synthesizer-2
Model: 394-08
ROM version: 2.00

Sequence name: htpan08 157-s
Sequence: CCA AAC ATA CTT TCG ATT TCA GGA GG

Cycle: 40 nM CE

End procedure: End CESS
DMT: Off

POl

Comments: 1:250 Dilution

$OD_{260} = 0.1479$

$OD_{280} = 0.0885$

$OD_{260}/280 = 1.6688$

DNA

$0.1479 \times 250 \times 33 = 1.22 \, \mu g/\mu l.$

$(26)(330) = 8580$

$(1.22 \mu g/\mu l)/8580) \times 10^6 = 142.2 \, pmol/\mu l$

18

Human Genome Sciences, Inc.

Plate I.D. _Misc. DT/pP_

Date Initiated: _9/23/93_

Date Completed: _9/26/93_

Results Folder: _09/25/93 05_

% Good: _16/27_

Templates	Sequence Reaction	Gel Run
Method: _Misc_	Method: _Manual_	Machine ID: _05_
Prep Person: _Gly, JW, Sm, Amk, DB, YFW_	Prep Person: _Ming_	Gel Loader: _Ming_
Prep Date: _9/22/93_	Prep Date: _9/24_	Run Date: _9/24_

	#	Sample Name	Chemistry DP/DT	Primer Name	\multicolumn{4}{c}{Signal Strength}	Rate Spacing	Vector	Edited Length	# N's	Wash Code
					C	A	G	T					
	1	PGEM DTest 1	DT	M13-21	255	169	160	82	9.71		350	1	
-ly	2	SOD19 A00474a		474	–	–	–	–	–	–	–	–	N
	3	B00474a			–	–	–	–	–	–	–	–	N
	4	C00474a			31	33	30	39	–12				R
	5	D00474a			35	37	28	35	–12				R
	6	E00474a			120	75	71	41	9.78				R
	7	F00474a			–	–	–	–	–	–	–	–	N
	8	G00474a			86	62	47	49	–12				R
	9	H00474a			–	–	–	–	–	–	–	–	N
JW Amk	10	ZFBR211 00232		232	48	50	34	40	9.89	–	350	9	
	11	H1BEC69 00680		680-S	558	438	288	210	9.90		530	6	
	12	HE8AY29 00202		202-S	29	32	29	32	9.69	–	–	-	R
	13	HTPAN9 800157		157-S	404	762	381	122	9.92		350	6	
Sm	14	HH PBF73 00001		P1	584	464	625	191	9.93		450	6	
	15	HE8AE45 00002		P2	40	32	25	26	9.79	–	-	-	R
	16	HE8AE45 00004		P4	132	206	192	49	9.93		470	8	
	17	HHPBF73 00508		P508	396	530	608	102	9.89		410	3	
	18	HHPBF73 00509		P.509	337	480	424	117	9.88		520	4	
DB	19	HLFCD44 00689		689	–	–	–	·	–	–	–	–	N
YFW	20	PGEM & 38P	DP	Rev-	338	252	197	172	10.06		460	5	
	21	HCAHA 02 Ra			364	275	170	119	10.11		460	10	
	22	HTYSE 16 Ra			89	199	110	97	10.01		530	5	
	23	HE7SE 81 Ra			270	192	114	81	10.03		610	8	
	24	HCAHA 02 Fa	DP	FOR	409	288	154	56	9.97		480	5	
	25	HE7SE 81 Fa			544	335	203	118	10.01		570	9	
	26	HTYSE 16 Fa			116	72	36	28	9.91		390	2	
	27	PGEM & 38F			320	82	132	83	9.95		500	10	
	28												
	29												
	30												
	31												
	32												

~60 < poly

Analyzed by: _ASP_

Factura/Blast Analysis: _____

Additional Comments: RE-TRACTED

19

Human Genome Sciences, Inc.

Plate I.D. __Misc DP__

Date Initiated: __9/23/93__

Date Completed: __9/25/93__

Results Folder: __09/25/93 DNA 11__

% Good: __18/30__

	Templates		Sequence Reaction		Gel Run
Method:	Misc.	Method:	Manual	Machine ID:	11
Prep Person:	AMK, JW	Prep Person:	Debbie	Gel Loader:	Debbie
Prep Date:	9/25/93	Prep Date:	9/24	Run Date:	9/24

#	Sample Name	Chemistry pPDT	Primer Names	Signal Strength C	A	G	T	Base Spacing	Vector	Edited Length	Gel #	Track Code
1	PGEM F 451-021 1-33F(+)	DP	FOR							440	1	
AMK 2	DNase P F											N
3	HIBEC69F									540	22	
4	HIBCW23F									300		T
5	HE8AY29F									300		T
√ 6	HTPAN08F									350		T
JW 7	HFLBM01F											R
8	02F									360		
9	03F											T
10	04F											T
11	05F											R·
12	06F											T
13	07F											R
14	08F											A,R
√ 15	09F		√									T
AMK 16	DNase P R		REV									R
17	HIBEC69R									400	2	
18	HIBCW23R									500	2	
19	HE8AY29R									370		
√ 20	HTPAN08R									290	32	M
JW 21	HFLBM01R									30	2	
22	02R									350	5	
23	03R									320	2	
24	04R									260	12	
25	05R									370	20	
26	06R									150	4	
27	07R											R
28	08R											R
√ 29	09R									260	15	
(6) 30	PGEM R 451-032 3F(+)		√							385	10	
31												
32												

Analyzed by: _____

Factura/Blast Analysis: _____

Additional Comments:

20

Applied Biosystems

Synthesis Order - 5426 HTPAN08r - 66s

Run date: 2/3/94
Run ID: 5426 AMK
Customer: Ann Kim

1.   KH
2.
Synthesizer: Synthesizer-2
Model: 394-08
ROM version: 2.00

Sequence name: 5426 HTPAN08r - 66s
Sequence: CAT CAA GGA GTG GGC ATT C

Cycle: 40 nM CE

End procedure: End CESS
DMT: Off

POS

Comments:

RPD

21

Applied Biosystems

RP03

Synthesis Order - 5424

Run date: 2/3/94
Run ID: 5424 AMK
Customer: Ann Kim

1.   KH
2.
Synthesizer: Synthesizer-2
Model: 394-08
ROM version: 2.00

Sequence name: 5424 HTPAN08F - 318s
Sequence: GGT GCC TCT TCT CTC TTT TG

Cycle: 40' nM CE

End procedure: End CESS
DMT: Off

P03

Comments:

Sent to "Synthesizer-2" col. 2 seq 32 at 2/3/94 2:57 PM.

Applied Biosystems

Synthesis Order - 5425 HTPAN08R - 404s

Run date: 2/3/94
Run ID: 5425 AMK
Customer: Ann Kim

1.   KH
2.
Synthesizer: Synthesizer-2
Model: 394-08
ROM version: 2.00

Sequence name: 5425 HTPAN08R - 404s
Sequence: GAG CAC TTG ATA GAC CAT G

Cycle: 40 nM CE

End procedure: End CESS
DMT: Off

P04

Comments:

23

Human Genom Sciences, Inc.

Plate I.D. __misc DT__

Date Initiated: __2/8/94__

Date Completed: _____

Results Folder: __HGS 47 2/9/94__

% Good: __DT 11/20__

	Templates		Sequence Reaction		Gel Run
Method:		Method: _Manual_		Machine ID: _47_
Prep Person:		Prep Person: _JMA_		Gel Loader: _JMA_
Prep Date:		Prep Date: _2/8/94_		Run Date: _2/8/94_

#	Sample Name	Chemistry DP/DT s	Primer Name	Signal Strength C	A	G	T	Base Spacing	Vector	Edited Length	% Ns	Trash Code
1		DT										
2	PGEM DT			148	263	421	156	10.59	5	465	4N	
3	PD10 HCT 7311 SDS			26	83	103	43	11.02	10	340	8N	
4	PD10 HCT 7312 SDS											N
5	PD10 HCT 7313 SDS			17	46	52	23	11.20	10	290	8N	
6	PD10 HCT 7314 SDS											N
7	HJBAVGC P589			45	109	131	58	10.54	40	360	3N	
8	HJBAVGC P5317			36	158	133	44	10.57	40	420	13N	
9	HIBEJ 895 36 FP03											N
10	HIBEJ 895 36 RP03											N
11	HIBEJ 895 36 RP2											N
12	HIBEJ 895 36 RP1											N
13	HIBEJ 895 36 FP											N
14	HIBEJ 895R P1											N
15	HIBEJ 895 P1											N
16	HIBEJ 895 RP21											N
17	HIBEJ 895 RP03			48	54	57	48	10.92	40	380	5N	
18	HIBEJ 895 FP03S			44	44	45	47	10.51	40			L
19	HIBEJ 895 FP03											N
20	HIBEC 695 FP01											N
21	HIBEC 695 RP01											N
22	HIBEC 695 FP03			81	71	34	75	-12				RC
23	HTISO42RP1b			97	208	316	130	-12				RC
24	HIBEH G4RP01											N
25	HIBEH G4RP02			70	100	163	48	10.76	40	400	3N	
26	HIBEH G4 RP03			91	72	131	37	10.95	50	280	22N	
27	HTPAN08 RP03			147	50	161	88	10.85	30	270	3N	
28	HTPAN08 RP04											N
29	HTPAN08 RP05			194	757	446	337	10.53	10	390	12N	
30	HE7SE29RP01			36	65	42	52	10.51				m
31	HPRAL82 RP01b			48	170	254	121	10.71	40	400	5N	
32												

Analyzed by: _____

Factura/Blast Analysis: _____

Additional Comments: { samples in brackets – not enough for a seq. reac – please resubmit

Human Genon. Sciences, Inc.

Plate I.D. _mwc dt's #2_

Date Initiated: _2/12/94_

Date Completed: _2/13/94_

Results Folder: _HGS 472.139_

% Good: _18132   56%_

	Templates		Sequence Reaction		Gel Run	
Method:	Mw.	Method:	Manual	Machine ID:	47	
Prep Person:		Prep Person:	DMD	Gel Loader:	DMD	
Prep Date:		Prep Date:	2.13.94	Run Date:	2.13.94	

#	Sample Name	Chemistry DP/DT	Primer Name	Signal Strength C	A	G	T	Base Spacing	Vector	Edited Length	% Ns	Trash Code
1	HGEN1 DT	DT		461	309	178	153	10.07	≈20	350	2N	
2	HEL BG 45 RPC1		RPC1									N
3	HSBA T63 b RPC1		1471	417	259	167	150	10.60	≈20	390	1N	
4	" & RPC1		1471	365	233	165	138	10.02	≈20	400	3N	
5	HETA0 67 NP 20		5454									N
6	HLTALV 73 RP11		5455	155	125	77	38	10.04	≈30		7N	
7	" EP7		5479									N
8	H PRTK 45 RPC1		5470	525	308	174	131	10.16	≈20	420	2N	
9	" h RP02		5471	428	273	166	177	10.12	≈40	410	0N	
10	HLTALV 73 P12		5483	120	55	42	24	10.08	≈30	270	8N	
11	HETA0 67 RP 10b		5465	122	82	44	31	10.13				many N's
12	" EP0 6b		5461	101	79	51	35	10.16	≈40	310	11N	
13	" EP01		5370	148	86	54	50	10.23	≈20	290	5N	
14	" FP11b		5473	109	76	45	43	10.14				many N's
15	HLTALV 73 RP03b		53EB	30	42	58	25	-12				R
16	HLTALV 73 FP15		53EC									N
17	HETAL 41 FP01		3473	153	175	154	106	-12				R
18	HTPANV9 RP03a		3195	478	389	365	95	10.02	≈30	290	0N	
19	" RPC4a		4245									N
20	" RPC5a		663	269	164	161	73	10.21	≈40	300	6N	
21	HP7SE 24 RP02a		5465									N
22	HPRAL 45 RP01c		2235	240	145	78	62	10.17	≈50	330	1N	
23	HETPA 3 FP02		5407	243	172	110	85	10.08	≈20	250	6N	
24	" FP03		FP03	466	310	225	159	10.17	≈40	300	1N	
25	" FP04		5704	634	269	172	128	10.23	≈50	310	2N	
26	" FP05		FP05	415	195	116	103	10.14	≈50	330	4N	
27	" RP04		RP04	434	309	165	173	10.39	≈30	220 A	2N	*
28	" RP05		RP05	177	158	76	69	10.29	≈50	300	3N	
29	HLFBE 105 06 RP1C		5415	59	48	26	20	10.26				many N's
30	RP1Ca		5415	69	50	27	20	10.34				many N's
31	HLFBE 105 06 RP11		5411									N
32	RP11	DT	5411									N

Analyzed by: _A SP_

Factura/Blast Analysis: _____

Additional Comments: _* #27 → 250 bases then poly A's_

uploaded Scientist + Full length

ab Applied Biosystems

Synthesis Order - 5688 HTPAN08F 488-AP07

Run date: 3/3/94
Run ID: 5688
Customer: A KIM

1.   CX
2.
Synthesizer: Synthesizer-2
Model: 394-08
ROM version: 2.00

Sequence name: HTPAN08F 488-AP07
Sequence: CTG CTA GCA AAC TGA TAT GAG

Cycle: 40 nM CE

End procedure: End CESS
DMT: Off

Comments:
 Sent to "Synthesizer-2" col 4 seq 34 at 3/8/94 2:07 PM.

26

Applied Biosystems

Synthesis Order – 5676 HTPAN08   333-SP06

Run date: 3/3/94
Run ID: 5676 AK
Customer: A KIM

1.   JPW
2.
Synthesizer: Synthesizer-1
Model: 394-08
ROM version: 2.00

Sequence name: 5676 HTPAN08   333-SP06
Sequence: GGG GGA ATA TTT GAG CTT AAG G

Cycle: 40 nM CE

End procedure: End CESS
DMT: Off

Comments:
   Sent to "Synthesizer-1" col 2 seq 32 at 3/7/94 8:27 AM.

27

Human Genome Sciences, Inc.   Plate I.D.(s) __DP'S REV_____ _____

Date Initiated: 3/10/94 _____   Results Folder: _HGS 50 3/11/94_

Date Completed: 3/11/94 _3/11/44_   % Good: _21/28_   % Good: ___

Templates	Sequence Reaction	Gel Run
Method: ————	Method: MANUAL/BIOMEK	Machine ID: 50
Prep Person: MISC	Prep Person: BCI	Gel Loader: TAL
Prep Date: ————	Prep Date: 3/10/94	Run Date: 3/10/94

#	Sample Name	Scientist name/init control	Primer DP/DT DP R	Signal Strength C	A	G	T	Base Spacing	Vector	Edited Length	% Ns	Trash Code
1	PGEMR			374	254	155	99	9.92	85	200	1	
2	HHPEB36R	HLI		245	161	96	50	9.97	96	234	12	
3	HOSAA70R	HLI		193	145	63	61	10.09	105	295	3	
4	HPBEC27R	HLI		188	135	59	57	9.51	101	300	9	
5	HLTAI45R	HLI		254	185	81	60	10.02	93	307	4	
6	HE9DR66R	HLI		92	51	41	45	9.50	9C			R
7	HMPTE39R	HLI		214	132	55	53	10.05	100	280	2	
8	HLTBX37R	T. Curtis										N
9	HTPAN08S01R	ANN KIM		125	135	47	39	10.21	110	260	4	
10	HTPAN08S02R	ANN KIM		191	131	59	59	9.93	104	226	3	
11	HTPAN08S03R	ANN KIM		57	102	45	40	9.88	103			m
12	HTPAN08S04R	ANN KIM		216	170	65	60	10.06	105	275	3	
13	HTPAN08S05R	ANN KIM		331	270	83	87	9.97	98	272	2	
14	HTPAN08S06R	ANN KIM		204	222	80	71	9.54	95	235	4	
15	HTPAN08S07R	ANN KIM		116	72	37	33	9.52	105	215	4	
16	HTPAN08S08R	ANN KIM		150	102	46	42	9.94	109	212	7	
17	HTPAN08S09R	ANN KIM		100	102	43	34	10.00	165	245	4	
18	HTPAN08S10R	ANN KIM										N
19	HTPAN08S11R	ANN KIM		231	197	74	73	10.13	99	255	3	
20	HTPAN08S12R	ANN KIM		214	154	57	52	9.99	102	268	1	
21	HTPAN08S13R	ANN KIM		140	108	75	58	10.03	90			R
22	HTPAN08S14R	ANN KIM		209	179	75	61	9.98	99	271	4	
23	HSABH13S05R	ANN KIM		130	116	39	37	10.09	105	295	4	
24	HETDE26R	SUK		209	106	70	58	10.02	99	230	2	
25	HFGAN12R	SUK										N
26	HATBG78R	SUK		201	229	57	104	10.09	94	300	2	
27	HHPI84R	SUK		247	154	59	131	10.17	92	288	6	
28	HHPEC49S3RA	SUK										N
29												
30												
31												
32												

Analyzed by: _JMD_   Factura/Blast Analysis: _____

Uploaded by: _✓_   Folder: _Full length + scientist_

Additional Comments:

28

Plate I.D.(s) __DT's #2__

Date Initiated: __3|8|94__

Date Completed: __3/9/94__

Results Folder: __HGS 43   3/9/94__

% Good: _____   % Good: _____

Templates		Sequence Reaction		Gel Run	
Method:		Method: MANUAL		Machine ID: 4 3	
Prep Person:		Prep Person: CDL		Gel Loader: BCI	
Prep Date:		Prep Date: 03/08/94		Run Date: 3|8|94	

#	Sample Name	Scientist name/init control	Primer DP/DT DT	Signal Strength C	A	G	T	Base Spacing	Vector	Edited Length	% Neg	Trash Code
1	PGEDMDT											N
2	HIBEC69S07RP04	ANN KIM	672	—								N
3	HIBEC69S08RP04	ANN KIM	672	29	25	8	61	72-00	—	—		L
4	HIBEC69S09RP04	ANN KIM	672									N
5	HIBEC69S10RP04	ANN KIM	672	—								N
6	HIBEC69S11RP04	ANN KIM	672	—								N
7	HIBEC69S12RP04	ANN KIM	672	—								N
8	HIBEC69S13RP04	ANN KIM	672	—								N
9	HIBEC69S14RP04	ANN KIM	672									N
10	HIBEC69S15RP04	ANN KIM	672									N
11	HIBEC69S16RP04	ANN KIM	672									N
12	HIBEC69S17RP04	ANN KIM	672									N
13	HIBEC69S18RP04	ANN KIM	672	244	159	160	75	10.77	20	330	3	
14	HIBEC69RP04	ANN KIM	672	—								N
15	HTPAN08S01RP03	ANN KIM	5424	—								N
16	HTPAN08S02RP03	ANN KIM	5424									N
17	HTPAN08S03RP03	ANN KIM	5424	38	111	139	111	10.87	10	500	3	
18	HTPAN08S04RP03	ANN KIM	5424	106	313	356	350	10.94	10	550	2	
19	HTPAN08S05RP03	ANN KIM	5424									N
20	HTPAN08S06RP03	ANN KIM	5424	365	441	181	595	-12.00	—			R / SFd3
21	HTPAN08S07RP03	ANN KIM	5424									N
22	HTPAN08S08RP03	ANN KIM	5424	—								N
23	HTPAN08S09RP03	ANN KIM	5424									N
24	HTPAN08S10RP03	ANN KIM	5424	—	—	—						N
25	HTPAN08S11RP03	ANN KIM	5424	—								N
26	HTPAN08S12RP03	ANN KIM	5424	—								N
27	HTPAN08S13RP03	ANN KIM	5424	41	139	155	129	10.86	10	420	4	
28	HTPAN08S14RP03	ANN KIM	5424	212	258	212	248	10.69	10	400	3	
29	HTPAN08RP03	ANN KIM	5424									N
30	HRGBF22RP01	BEDNARI	5618	—								N
31	HHPEC49S13RP12	SUK		—								N
32	HHPEC49S13FP12	SUK		—								N

Retracked Seal

Analyzed by: __Seal__

Uploaded by: _____   Folder: __full length/__

Factura/Blast Analysis: _____

scientist

all samples being redone in Seq.

Human Genome Sciences, Inc.

Plate I.D.(s) __DT'S #2__

ute Initiated: __3/8/94 Redos__   Results Folder: __43 HGS 3/10/94__

Date Completed: _____   % Good: __3/24__ % Good: __2/19__

Templates	Sequence Reaction	Gel Run
Method:	Method: MANUAL	Machine ID: 43
Prep Person:	Prep Person: CDL	Gel Loader: BCI
Prep Date:	Prep Date: 03/08/94	Run Date: 3/10/94

#	Sample Name	Scientist name/init control	Primer DP/DT DT	C	A	G	T	Base Spacing	Vector	Edited Length	% Ns	Trash Code
1	PGEDMDT			2H	13	110	14	10.45	50	450	4	
2	HIBEC69S07RP04a	ANN KIM	672	-								N
3	HIBEC69S08RP04a	ANN KIM	672	⌐								N
4	HIBEC69S09RP04a	ANN KIM	672	8	18	52	23	-12.00	-			R
5	HIBEC69S10RP04a	ANN KIM	672	6	15	34	16	10.15	-			R
6	HIBEC69S11RP04a	ANN KIM	672	7	16	36	17	10.52				R
7	HIBEC69S12RP04a	ANN KIM	672	-								N
8	HIBEC69S13RP04a	ANN KIM	672	-								N
9	HIBEC69S14RP04a	ANN KIM	672									N
10	HIBEC69S15RP04a	ANN KIM	672									N
11	HIBEC69S16RP04a	ANN KIM	672	-								N
12	HIBEC69S17RP04a	ANN KIM	672	-								N
13	HIBEC69S18RP04a	ANN KIM	672									N
14	HIBEC69RP04a	ANN KIM	672	53	23	71	263	10.16	-			H
15	HTPAN08S01RP03a	ANN KIM	5424	-								N
16	HTPAN08S02RP03a	ANN KIM	5424	-								N
17	HTPAN08S03RP03a	ANN KIM	5424	723	149	239	71	10.23	17	300	1	
18	HTPAN08S04RP03a	ANN KIM	5424	202	189	155	67	9.80	60	300	1	
19	HTPAN08S05RP03a	ANN KIM	5424	-								N
20	HTPAN08S06RP03a	ANN KIM	5424	-								N
21	HTPAN08S07RP03a	ANN KIM	5424	-								N
22	HTPAN08S08RP03a	ANN KIM	5424	⌐								N
23	HTPAN08S09RP03a	ANN KIM	5424	⌐								N
24	HTPAN08S10RP03a	ANN KIM	5424	-								N
25	HTPAN08S11RP03a	ANN KIM	5424	-								N
26	HTPAN08S12RP03a	ANN KIM	5424	-								N
27	HTPAN08S13RP03a	ANN KIM	5424	195	28	168	84	10.14	10	420	1.5	
28	HTPAN08S14RP03a	ANN KIM	5424	326	398	413	103	10.07	10	300	1	
29	HTPAN08RP03a	ANN KIM	5424	-								N
30	HRGBF22RP01a	BEDNARI	5618	-								N
31	HHPEC49S13RP12a	SUK		-								N
32	HHPEC49S13FP12a	SUK		-								N

Ketracked : SPK

Analyzed by: __L. KD__   Factura/Blast Analysis: _____

Uploaded by: __✓__ Folder: _____

"Full Length"

"Sc. Seq."

30

Human Genome Sciences, Inc.

Plate I.D.(s) __MSc DT__

ate Initiated: _____

Date Completed: _____

Results Folder: __HGS 04 3|10|94__

% Good: __9/32__   % Good: _____

Templates	Sequence Reaction	Gel Run
Method:	Method: Manual	Machine ID: 4
Prep Person:	Prep Person: WMC	Gel Loader: WMC
Prep Date:	Prep Date: 3.9.94	Run Date: 3|10|94

#	Sample Name	Scientist name/init control	Primer DP/DT DT	Signal Strength C	A	G	T	Base Spacing	Vector	Edited Length	% Ns	Trash Code
1	PGEM DT			174	125	83	76	10.49	20	360	.8	
2	HALSK38S16RP04	Ann Kim	5677									N
3	HALSK38S17RP04	Ann Kim	5677									N
4	HALSK38S18RP04	Ann Kim	5677									N
5	HALSK38S19RP04	Ann Kim	5677									N
6	HALSK38S20RP04	Ann Kim	5677	42	39	51	40	-12.00				R
7	HALSK38S21RP04	Ann Kim	5677									N
8	HALSK38S22RP04	Ann Kim	5677									N
9	HALSK38S23RP04	Ann Kim	5677									N
10	HALSK38S24RP04	Ann Kim	5677									N
11	HALSK38S25RP04	Ann Kim	5677									N
12	HALSK38RP04	Ann Kim	5677									N
13	HKMAAS1RPO2	Ann Kim	5678									N
14	HKMAAS1RPO1b	Ann Kim	5496									N
15	HTPANO8RPO6	Ann Kim	5676	140	374	113	76	10.40	35	335	1.5	
16	HE8AY29RP03	Ann Kim	5675	207	244	251	138	10.53	10	350	1.6	
17	HAPATPD10 P01	Ann Kim	PD3'	285	49	164	114	10.61	25	365	1.6	
18	MCPSCPD10 P01	Ann Kim	PD3'	229	241	179	202	10.36	20	300	1.0	
19	HPLAJ24S11RPO2	JM 5.22	5671									N
20	HPLAJ24S11FPO1	JM	5672	48	24	18	19	10.32	20	230	6.5	.
21	HPLAJ24S26FPO1	JM	5672	65	24	23	26	10.36	20	320	2.2	
22	HPLAJ24S32FPO1 39 FPO1	JM	5672									N
23	HPLAJ24S39FPO1 32 FPO1	JM	5672	80	61	45	50	10.43	15	35	1.3	.
24	STCMTO2Rp01a	QQZ	1548									N
25	STCMTO2Rp01b	QQZ	1549									N
26	STCMTO3Rp01a	QQZ	1548									N
27	STCMTO3RP01b	QQZ	1549									N
28	STCMTO6RP01a	QQZ	1548									N
29	STCMTO6RP01b	QQZ	1549	53	53	33	23	10.41	50	270	1.9	
30	STCMTO7RP01a	QQZ	1548									N
31	STCMTO7RP01b	QQZ	1549									N
32	STCMTO8RP01a	QQZ	1548									N

Analyzed by: __JPF__

Uploaded by: __JF__   Folder: __Scientists Folder__

Factura/Blast Analysis: _____

Additional Comments: full length

31

Human Genome Sciences, Inc.

Plate I.D.(s) _Fwd #1 / rev_

Date Initiated: 3/12/94

Date Completed: 3/13/94

Results Folder: HGS 38 3/13/94

% Good: 2/32 - 62%   % Good: _____

Templates	Sequence Reaction	Gel Run
Method:	Method: Manual	Machine ID: 38
Prep Person:	Prep Person: DMD	Gel Loader: KMC
Prep Date:	Prep Date: 3/12/94	Run Date: 3/12/94

	#	Sample Name	Scientist name/init control	Primer DP/DT DP For	C	A	G	T	Base Spacing	Vector	Edited Length	#Ns	Trash Code
A1	1	pgemf			549	326	150	192	9.24	54	670	3	
b1	2	BMP01F	JPW	Forwa	190	77	107	72	-12.00	-	.		R
C1	3	BMP02F	JPW	Forwa	257	201	174	169	9.43		105-290	6	
D1	4	BMP03F	JPW	Forwa	365	172	163	164	9.45		105-365	9	
E1	5	BMP06F	JPW	Forwa	250	158	141	127	-12.00	--	-	-	R
F1	6	BMP07F	JPW	Forwa	279	40	51	119	9.65		-	-	H
G1	7	BMP08F	JPW	Forwa	334	152	155	122	9.47		93-290	13	
H1	8	BMP09F	JPW	Forwa	279	125	135	134	9.42		60-	-	L
A2	9	BMP10F	JPW	Forwa	252	114	169	106	-12.00	-	-	-	R
b2	10	BMP11F	JPW	Forwa	266	176	106	121	9.64		111-285	11	
C2	11	BMP12F	JPW	Forwa	298	192	135	173	9.43		105-440	10	
D2	12	BMP13F	JPW	Forwa	392	206	169	120	9.30		95-440	15	
E2	13	BMP14F	JPW	Forwa	501	223	156	179	9.36		100-520	7	
F2	14	BMP15F	JPW	Forwa	661	238	135	174	9.65		100-430	8	
G2	15	BMP16F	JPW	Forwa	96	165	118	55	9.52		-	-	M
H2	16	BMP17F	JPW	Forwa	122	76	38	30	-12.00	-	-	-	R
A3	17	BMP18F	JPW	Forwa	337	196	144	123	9.48		95-440	12	
b3	18	BMP19F	JPW	Forwa	137	74	50	40	9.49		-	-	R
C3	19	BMP20F	JPW	Forwa	53	30	30	23	-12.00	-	-	-	H
D3	20	HPLAJ24S11F	JM (T22r)	Forwa	169	81	47	43	9.26	43	70-355		25polys
A10	21	HL1SB62Fa	D.KOZAK	Forwa		NO	ANALYZED	DATA					N
A5	22	PGEMR	control	DP rev	503	342	225	183	9.43	77	670	5	
b5	23	HFSBC6527R	PLHUDSO	REV	90	47	51	36	-12.00	105	-	-	SFS
C5	24	HFSBC6533R	PLHUDSO	REV		NO	ANALYZED	DATA					N
D5	25	HUKBA46Ra	D.KOZAK	Rever	371	119	159	138	9.45	103	400	8	
E5	26	HTPAN08S03R	ANN KIM	Rever	225	169	91	76	9.30	105	190	10	
F5	27	HTPAN08S04R	ANN KIM	Rever	439	285	167	111	9.44	107	550	8	
G5	28	HTPAN08S13R	ANN KIM	Rever	119	68	60	46	9.40	110	130-450		20pcly?
H5	29	HTPAN08S14R	ANN KIM	Rever	266	217	124	102	9.63	106	405	4	
A6	30	HOSAB71Ra	ANN KIM	Rever	127	131	58	76	9.34	104	460	.	
b6	31	HE9MF72AR	ANN KIM	Rever	80	87	59	43	9.32	107	460	2	
C6	32	HE9MF73BR	ANN KIM	Rever	104	83	44	36	9.33	107	455	1	

Analyzed by: D.J   Factura/Blast Analysis: _____

Uploaded by: R.J   Folder: full length + scientists.

Additional Comments: All the BMP samples have strong fluorescence stops in between 70-100.

Human Genome Sciences, Inc.

Plate I.D.(s) _____ nucx dts # 2

Templates	Sequence Reaction	Gel Run
Method:	Method: Manual	Machine ID: 35
Prep Person:	Prep Person: DMD	Gel Loader: DMD
Prep Date:	Prep Date: 2/12/94	Run Date: 3/12/94

#	Sample Name	Scientist name/init control	Primer DP/DT DT	C	A	G	T	Base Spacing	Vector	Edited Length	% Ns	Trash Code
1	PGEMDT			446	334	228	281	9.15	≈10	380	0N	
2	HMPBB73RP01	H.LI	1031	32	63	29	57	-12				R
3	HMPBB73FP01	H.LI	1030	26	58	45	77	-12				R
4	HWFBD68FP01	H.LI	3-3	20	186	202	152	-12				R
5	HWFBD68RP01	H.LI	3-4	12	32	62	51	-12				R
6	HEPBO63RP01	D.KOZAK	53-9	122	127	67	82	9.04	≈10	230	4N	
7	HL1SB62RP01	D.KOZAK	53-3									N
8	HSABF11RP01	D.KOZAK	1339	174	142	84	77	9.11	≈20	230	8N	
9	HOSAB71RP03	ANN KIM	55-3	—								N
10	HOSAB71RP04	ANN KIM	5677	—								N
11	HOSAB71RP06	ANN KIM	5637	18	48	31	24	-12				R
12	HE9MF73ARP03	ANN KIM	54-3	—								N
13	HE9MF73BRP03	ANN KIM	55-3									N
14	HE9MF73ARP04	ANN KIM	5677	—								N
15	HE9MF73BRP04	ANN KIM	5677	—								N
16	HE9MF73ARP06	ANN KIM	5637	—								N
17	HE9MF73BRP06	ANN KIM	5637	18	50	29	23	-12				many Ns
18	HTPAN08RP06	ANN KIM	56-5	243	723	285	204	9.04	≈40	340	2N	
19	HTPAN08RP07	ANN KIM	5633	474	424	655	204	9.12	≈50	240	8N	
20	MCPSCPD10P02	ANN KIM	PD 3	419	613	492	484	-12	≈90	180	3N	
21	HAPATPD10P02	ANN KIM	PD 3	384	512	280	290	9.12	≈30	260	9N	
22	HPLBTS2ARP01	ANN KIM	5635	287	400	293	157	9.00	≈130	280	2N	
23	HPLBTS2BRP01	ANN KIM	5635	242	301	199	125	9.10	≈10	300	6N	
24	HE2BG16RP01	ZHEN LI	1424	—								N
25	HE2BG16FP01	ZHEN LI	1422	—								N
26	HE2BG16RP02	ZHEN LI		269	260	210	121	9.11	≈20	270	2N	
27	HASSB35S08FP05	ZHEN LI	5634	122	91	44	61	9.06	≈40	200	11N	
28	HHPEC49S03FP14A	SUK		155	167	117	64	9.06	≈20	370	6N	
29	HHPEC49S03RP14A	SUK		113	63	58	66	9.12	≈80	250	1N	
30	HHPEC49S03FP15	SUK		50	46	42	20	9.14	≈50	150	4N	
31	HHPEC49S03RP15	SUK		57	71	49	30	9.05				many Ns
32	HSSAW84S02P01	YWEI		92	95	79	53	9.09	≈50	300	4N	

33

Synthesis Order - 5756 HTPAN08R 124A-P08

Run date: 3/11/94
Run ID: 5756 AMK
Customer: Ann Kim

1.   KH
2.
Synthesizer: Synthesizer-2
Model: 394-08
ROM version: 2.00

Sequence name: 5756 HTPAN08R 124A-P08
Sequence: CTG GTC AAG TGG TAA GGA G

Cycle: 40 nM CE

End procedure: End CESS
DMT: Off

Comments:

34

Human Genome ~ences, Inc.

Date Initiated: 3/18/94 _____

Date Completed: _____

Results Folder: _TGS 10 3/19/94_

% Good: _17/30_ % Good: _____

	Templates		Sequence Reaction		Gel Run	
Method:		Method:		Machine ID:	10	
Prep Person:		Prep Person:		Gel Loader:	SURA	
Prep Date:		Prep Date:		Run Date:	3/18/94	

#	Sample Name	Scientist name/init	Primer DP/DT	Signal Strength				Base Spacing	vector	Edited length	% Ns	Trash Code
				C	A	G	T					
1-A9	PGEMDT	CONTRO		89	287	575	82	10.31		550	0	
2-B9	7TMD126ARP01	ANN KIM	5780	>	NO	DATA						N
3-C9	7TMD126BRP01	ANN KIM	5780									N
4-D9	7TMD127ARP01	ANN KIM	5781	19	21	42	16	-12				R|L
5-E9	7TMD127BRP01	ANN KIM	5781									N
6-F9	7TMD130ARP01	ANN KIM	5782									N
7-G9	7TMD130BRP01	ANN KIM	5782		NO	DATA						N
8-H9	7TMD134BRP01	ANN KIM	5783									N
9-A10	7TMD136ARP01	ANN KIM	5784									N
10-B10	7TMD137ARP01	ANN KIM	5785	13	22	37	15	9.2				R|L
11-C10	7TMD137BRP01	ANN KIM	5785	35	98	98	27	10.15		370	4%	
12-D10	7TMD139ARP01	ANN KIM	5786	64	101	122	44	10.41		350	2%	
13-E10	7TMD139BRP01	ANN KIM	5786	30	69	98	35	10.39		350	<19.	
14-F10	HTPAN08S03RP08	ANN KIM	5756		NO	DATA						N
15-G10	HTPAN08S03RP08 H-704	ANN KIM	5756		NO	DATA						N
16-H10	HTPAN08S13RP08	ANN KIM	5756		NO	DATA						N
17-A11	HTPAN08S14RP08	ANN KIM	5756		NO	DATA						N
18-B11	HTPAN08RP08	ANN KIM	5756		NO	DATA						N
19-C11	HSCBB75S03RP01a	MAC	5731	87	177	221	106	10.35		370	2%	
20-D11	HSCBB75S03RP01b	MAC	5731	76	158	166	89	10.29		370	1%	
21-E11	HSCBB75S03RP02a	MAC	5732	120	290	273	83	10.40		370	4%	
22-F11	HSCBB75S03RP02b	MAC	5732	120	209	234	76	10.34		350	4%	
23-G11	HSCBB75S03RP03a	MAC	5734	116	286	282	141	10.51		300	1%	
24-H11	HSCBB75S03RP03b	MAC	5734	70	152	187	85	10.51		360	1%	
25-A12	HSCBB75S03RP04a	MAC	5795	100	224	202	93	10.31		370	1%	
26-B12	HSCBB75S03RP04b	MAC	5795	108	224	218	97	10.26		380	2%	
27-C12	HSCBB75S03RP05a	MAC	5796	61	196	196	89	10.41		250	5%	
28-D12	HSCBB75S03RP05b	MAC	5796	63	134	154	80	10.47		250	5%	
29-E12	HSCBB75S03RP06a	MAC	5797	55	117	121	49	10.36		350	3%	
30-F12	HSCBB75S03RP06b	MAC	5797	51	100	131	45	10.40		350	3%	
31-G12												
32-H12												

Analyzed by: _Donna_   Factura/Blast Analysis: _____

Uploaded by: _Donna_ Folder: _SCI/Full length_   NO REDO's

Additional Comments:

For the 15 primer should be 04 G10 (o Scienan tube

Human Genome Sciences, Inc.

Plate I.D.(s) _manuels_

ate Initiated: _____

Results Folder: _07/22/94 17 HGS_

Date Completed: _7/22/94_

% Good: _50_   % Good: _____

Templates	Sequence Reaction	Gel Run	
Method:MISC	Method:BIOMEK/MANUAL	Machine ID:	_17_
Prep Person:MISC	Prep Person:ASP	Gel Loader:	_ASP_
Prep Date:MISC	Prep Date:07/21/94	Run Date:	_07/21/94_

#.	Sample Name	Scientist name/init.	Primer DP/DT	Signal Strength G	A	T	C	Base Spacing	Vector	Edited length	% N's	Trash Code
1-A1	PGEMDT	CONTRO	DT	99	164	139	89	9.52	50	390	0	
2-B1	HTPAN08S04RP01a	Ann Kim		168	698	178	63	9.50	70	240	2.9	
3-C1	HTPAN08S04RP03a	Ann Kim		228	218	300	56	9.59	70	240	.8	
4-D1	HTPAN08S04RP05a	Ann Kim		165	453	18	63	9.41	80	280	1.4	
5-E1	HTPAN08S04RP06a	Ann Kim		170	531	185	85	9.43	60	100	15	
6-F1	HTPAN08S04RP07a	Ann Kim		185	139	240	50	9.53	70	270	.33	
7-G1	HTPAN08S04RP09a	Ann Kim										N
8-H1	HTPAN08S04RP10a	Ann Kim		120	197	103	74	9.29	80	380	0	
9-A2	HTPAN08S04RP12a	Ann Kim		202	461	188	80	9.29	80	330	.6	
10-B2	HTPAN08S04RP14a	Ann Kim		217	141	221	85	9.44	70	330	.9	
11-C2	HTPAN08S04FP15a	Ann Kim		175	134	200	56	9.43	80	270	3.3	
12-D2	HTPAN08S13RP01a	Ann Kim		74	59	58	105	-12.00				R
13-E2	HTPAN08S13RP03a	Ann Kim										N
14-F2	HTPAN08S13RP05a	Ann Kim										N
15-G2	HTPAN08S13RP06a	Ann Kim										N
16-H2	HTPAN08S13RP07a	Ann Kim										N
17-A3	HTPAN08S13RP09a	Ann Kim		133	117	99	49	9.35	70	390	2.6	
18-B3	HTPAN08S13RP10a	Ann Kim										N
19-C3	HTPAN08S13RP12a	Ann Kim		21	49	57	62	-12.00				R
20-D3	HTPAN08S13RP14a	Ann Kim										N
21-E3	HTPAN08S13FP15a	Ann Kim										N
22-F3	HHCMF74FP11	SUK		239	260	176	113	9.35	80	360	.6	
23-G3	HHCMF74RP11	SUK		191	155	216	107	9.40	70	310	1.6	
24-H3	HHCMF74FP12	SUK		280	290	127	89	9.41	70	390	0	
25-A4	HHCMF74FP13	SUK		287	411	155	101	9.44	90	300	0.3	
26-B4	HHCMF74FP14	SUK		213	348	174	85	9.28	30	350	1.7	
27-C4	HHCMF74RP12	SUK		194	175	186	76	9.37	50	340	0.3	
28-D4	HHCMF74FP01B	SUK		224	218	250	80	9.46	20	400	0.3	
29-E4	HMS8X93FP01B	SUK		223	233	219	80	9.52	50	400	0.5	
30-F4	HNFAG09FP01B	SUK		87	66	51	31	9.62	40	480	0.6	
31-G4	HP16A2A	Laurie										N
32-H4	HP2A2D	Laurie										N

Retracked ASK

Analyzed by: _____

Uploaded by: _ASP_   Folder: _Full length + scientists_

Factura/Blast Analysis: _____

DT 1-3 ... ASP

36

Applied Biosystems

Synthesis Order - 6442 HTPAN08 SCREEN RP01

Run date: 5/4/94
Run ID: 6442
Customer: ANN KIM

RP02

1. CX
2.
Synthesizer: Synthesizer-1
Model: 394-08
ROM version: 2.00

Sequence name: HTPAN08 SCREENRP01
Sequence: GCA GAT GCA GGA CAA GTA C

Cycle: 40 nM CE

End procedure: End CESS
DMT: Off

Comments:
Sent to "Synthesizer-1" col 3 seq 33 at 5/5/94 10:19 AM.

Sequence
HTPAN08
504
514

RP10

37

```
$ type U03470.Tfasta


(Peptide) TFASTA of: U03470.Gp_All  from: 1 to: 278  May 5, 1994  11:39

 .OCUS      RNU03470_1 .
 DEFINITION Rattus norvegicus Fas antigen ligand mRNA, complete cds. Ligand
            for Fas antigen; A member of TNF-family; apoptosis-inducing
            capacity; typeII-transmembrane protein; ligand for receptor.
            NCBI gi: 440179.
 DATE       12-JAN-1994 . . .

  TO: contig1.seq  Sequences:       1  Symbols:     1,872  Word Size: 2


The best scores are:                                    frame init1 initn opt
 . .

 $1$Dual:[Hgs.Ruben]Contig1.Seq   REFORMAT of: Contig1.Seq...(3)   86   123   197
 $1$Dual:[Hgs.Ruben]Contig1.Seq   REFORMAT of: Contig1.Seq...(1)   32    32    54
 $1$Dual:[Hgs.Ruben]Contig1.Seq   REFORMAT of: Contig1.Seq...(6)   32    32    42
 $1$Dual:[Hgs.Ruben]Contig1.Seq   REFORMAT of: Contig1.Seq...(4)   31    31    50
 $1$Dual:[Hgs.Ruben]Contig1.Seq   REFORMAT of: Contig1.Seq...(5)   29    29    36
 $1$Dual:[Hgs.Ruben]Contig1.Seq   REFORMAT of: Contig1.Seq...(2)   28    28    35


 U03470.Gp_All
 $1$Dual:[Hgs.Ruben]Contig1.Seq

  REFORMAT of: Contig1.Seq  check: -1  from: 1  to: 1876  May 5, 1994  11:38
  (No documentation)

 CORES       Frame: (3) Init1: 86 Initn: 123 Opt: 197
             24.1% identity in 170 aa overlap

               90        100       110       120       130       140
 U03470 FFMVLVALVGMGLGMYQLFHLQKELAELREFTNHSLRVSSFEKQIANPSTPSETKKPRSV
                      : ::|  |  :| |:   ::   :::::::: :|
 Contig KSSGTPSARXKDDFENLXGNHFYSSRKATKYLSPSERKRSSESSSSHNWDQRKNNTLSSP
               180       190       200       210       220      230

               150       160        170       180       190         200
 U03470 AHLTGNPRSRSIPLEWEDT-YGTALISGVKYKKGGLVINEAGLYFVYSKVYFR-GQSCNS
            :  :::::  :|:|   :||::   |  :::|:::  ::|:|||:|  |:|::||::|||   .:: ::
 Contig NSKNEKALGRKIN-SWESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKE
               240       250       260       270       280       290


                  210       220       230       240       250
 U03470 QPLSHK---VYMRNF-KYPGDLVLMEEKKLN-YCTTGQIWAHSSYLGAVFNLTVADHLYV
         :: ::|      |: ::  :||: ::||::  :  :  :::::::    :| |  |::|:|: :|::  |
 Contig NTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRILV
               300       310       320       330       340       350


               260         270
 U03470 NISQLSLINFEESKTFFGLYKL
         :::::  ||:::::: :|||  :
 Contig SVTNEHLIDMDHEASFFGAFLVGXLTWKEKAITSKXLFSFQDDTLXRCFKKSDQNKQTEN
               360       370       380       390       400       410


 03470.Gp_All
 ,1$Dual:[Hgs.Ruben]Contig1.Seq

  REFORMAT of: Contig1.Seq  check: -1  from: 1  to: 1876  May 5, 1994  11:38
  (No documentation)
```

```
SCORES        Frame: (1) init1: 32 Initn: 32 Opt: 54
              14.2% identity in 120 aa overlap

              40          50          60          70          80          90
  U03470  PGQRRPPPPPPPPSPLPPPSQPPPLPPLSPLKKKDNIELWLPVIFFMVLV-ALVGMGLGM
                          |:  ::  :|:|:  :  :   :::  ::   :  |
  Contig  TLYCXXKVLEIVVGLKMQNMDSIPSIKGEYLSLRKMTEFWFLXQMSTXXTWTMKPVFSGP
              320         330         340         350         360         370

              100         110         120         130         140         150
  U03470  YQLFHLQKELAELREFTNHSLRVSSFEKQIANPSTPSETKKPRSVAHLTGNPRSRSIPLE
          ::|  :::  :   ::::  :    :|:   :|:    |  :::::  :  :   :::::|::   :
  Contig  FXLANXPGKKKQXPQSDYSVFRMIHYEDVSKNLTKTNKQKTENKKPSMQSEXSSHNQKIL
              380         390         400         410         420         430

              160         170         180         190         200         210
  U03470  WEDTYGTALISGVKYKKGGLVINEAGLYFVYSKVYFRGQSCNSQPLSHKVYMRNFKYPGD
                ::  ::::::|:    |  |    |:  :  ::|||::
  Contig  QHTLFXKXLTYPKKMK---LLKDLSGLYLISVCXQKSRRLSASKHXCNGYIFWLYNLHLV
              440         450       460         470         480


U03470.Gp_All
$1$Dual:[Hgs.Ruben]Contig1.Seq

  REFORMAT of: Contig1.Seq  check: -1  from: 1  to: 1876  May 5, 1994  11:38
  (No documentation)

SCORES        Frame: (6) Init1: 32 Initn: 32 Opt: 42
              34.8% identity in 23 aa overlap

              230         240         250         260         270
  U03470  EKKLNYCTTGQIWAHSSYLGAVFNLTVADHLYVNI-SQLSLINFEESKTFFGLYKL
                                  :|::|    |:::  |:  ||:  |  |
  Contig  PVPSGVNELDLEXMERPKASDFXFPXNVRSIYIHIYISLNFXVFDMSKNPFPLPXSLSET
              550         560         570         580         590         600

  Contig  HEENCVSFKDVNXMIETCT
              610       620


U03470.Gp_All
$1$Dual:[Hgs.Ruben]Contig1.Seq

  REFORMAT of: Contig1.Seq  check: -1  from: 1  to: 1876  May 5, 1994  11:38
  (No documentation)

SCORES        Frame: (4) Init1: 31 Initn: 31 Opt: 50
              16.7% identity in 102 aa overlap

                              10          20          30          40
  U03470                  MQQPVNYPCPQIYWVDSSATSP-WAPPGSVFSCPSSGPRGPGQ
                          |::::   |  :::::|::::  :  |::   |
  Contig  RHWGPNNCHLLLRNKQCHFWSTCPASASARWXSTRKLQPHRETAGALXRFTISTQVCPRL
              470         480         490         500         510         520

              50          60          70          80          90          100
  U03470  RRPPPPPPPPSPLPPPSQPPPLPPLSPLKKKD-NIELWL-PVIFFMVLVALVGMGLGMYQ
          :|  ||::|::   :  ::  ::|  ::|:||  :::  :::  |    :   :::  :  :::|
  Contig  VPPGPPSXPXTCQSLTAVSQPGSRLCPLGXMSLTXSKWRDQKPLIFNFHKMLEVYIYIYI
              530         540         550         560         570         580

              110         120         130         140         150         160
  U03470  LFHLQKELAELREFTNHSLRVSSFEKQIANPSTPSETKKPRSVAHLTGNPRSRSIPLEWE
          ::::  ::|    |:
  Contig  FLXIFESLICLKIHSLCPEAXVRHMKKTVFHLKMLIKXLKLVL
```

U03470.Gp_All
^1$Dual:[Hgs.Ruben]Contig1.Seq

 REFORMAT of: Contig1.Seq   check: -1   from: 1   to: 1876   May 5, 1994   11:38
 (No documentation)

SCORES   Frame: (5) Initl: 29 Initn: 29 Opt: 36
              11.1% identity in 27 aa overlap

```
         50          60          70          80          90         100
U03470 PPPPPSPLPPPSQPPPLPPLSPLKKKDNIELWLPVIFFMVLVALVGMGLGMYQLFHLQKE
                              :||  :::    :  :::    :  ::  |  ::
Contig DMRXSPERSFSNFIFLGXVSHFQNSVCCRIFWLWLLYSDCIEGFLFSVFCLFVLVRFFET
        170         180         190         200         210         220


         110         120         130         140        ·150         160
U03470 LAELREFTNHSLRVSSFEKQIANPSTPSETKKPRSVAHLTGNPRSRSIPLEWEDTYGTAL

Contig SSXCIILKTEXSLXGYCFFFPGQLANXKGPEKTGFMVHVYQVLICYRNQNSVIFLKLKYS
        230         240         250         260         270         280
```

U03470.Gp_All
1Dual:[Hgs.Ruben]Contig1.Seq

 REFORMAT of: Contig1.Seq   check: -1   from: 1   to: 1876   May 5, 1994   11:38
 (No documentation)

SCORES   Frame: (2) Initl: 28 Initn: 28 Opt: 35
              16.7% identity in 18 aa overlap

```
         160         170         180         190         200         210
U03470 EDTYGTALISGVKYKKGGLVINEAGLYFVYSKVYFRGQSCNSQPLSHKVYMRNFKYPGDL
                              :|  :::::::::|::|  ::
Contig MKMFQKIXPKQTNRKQKTKNPLCNLSRAATTKKFYNTHCSESDSLIPRKXNCXKIFQDST
        400         410         420         430        ·440         450


         220         230         240         250         260         270
U03470 VLMEEKKLNYCTTGQIWAHSSYLGAVFNLTVADHLYVNISQLSLINFEESKTFFGLYKL

Contig SYQFASRNLEDCQLPNINAMVTSSGFIIYTLXRLXKKAQQSISQVVYHSSSLQVSLRDNI
```

Applied Biosystems

Synthesis Order - 6445 HTPAN08S13R P01

Run date: 5/6/94
Run ID: 6445 AMK
Customer: ann kim

1.   KH
2.
Synthesizer: Synthesizer-1
Model: 394-08
ROM version: 2.00

Sequence name: 6445 HTPAN08S13 RP01
Sequence: TGT CTC ACT CAG GCT TCA G

Cycle: 40 nM CE

End procedure: End CESS
DMT: Off

RP01
RP09

Comments:

RP09

41

Human Genome ~iences, Inc.   Pl~ .D.(s) _____ _____

Date Initiated: 05/11/94 _____

Date Completed: _05/12/94_

Results Folder: _05/12/94 .x9 Hi5_ ✓

% Good: 13/26 = 50% % Good: ___

Templates	Sequence Reaction	Gel Run
Method:	Method: MANUALS	Machine ID: 19 4C
Prep Person:	Prep Person: JMA	Gel Loader: JMA
Prep Date:	Prep Date: 05/11/94	Run Date: 05/11/94

G A T C

#	Sample Name	Scientific name/init	Primer DP/DT	Signal Strength C	A	G	T	Base Spacing	% Vector	Edited Length	N#	Trash Code
A1	PGEM	control	DT	178	170	130	64	12.05	38	432	2N	
B1	SOL10F√a	A.Chopra		160	149	98	65	12.11	20	310	7N	
C1	SOL10R√ a	A.Chopra		—	—	—	—	—				N ＊
D1	TNFQE60NB1P01 a	A KIM		54	64	48	30	12.08	80	320	8N	
E1	TNFQE60NB2P01 a	A KIM		66	85	54	34	12.05	50	380	12N	
F1	TNFQE60NB3P01 a	A KIM		34	39	2C	21	11.91				K
G1	TNFQE60BN4P01 a	A KIM		72	87	5C	35	11.98	40	390	6N	
H1	TNFQE60BN5P01 a	A KIM		133	195	109	63	11.99	20	430	4N	
A2	TNFQE60BN6P01 a	A KIM		46	56	37	25	11.99	70	300	6N	
B2	HTPAN08S04RP01 c	A KIM		142	303	176	62	11.98	40	390	4N	
C2	HTPAN08S13RP01 a	A KIM		—	—	—	—	—				N ＊
D2	HTPAN08S14RP01 a	A KIM		107	224	129	48	12.01	40	390	5N	
E2	HPRBI22RP01 a	BEDNARI		65	85	69	32	12.03	48	378	5N	
F2	HFCSA70RP01 a	BEDNARI		—	—	—	—	—				N
G2	HSAID14RP01 a	BEDNARI		51	47	39	2C	12.09	50	250	5N	
H2	HLTAF30RP01 a	BEDNARI		54	80	65	40	11.99	50	180	2N	
A3	HLTBR87RP01 a	Bednarik		—	—	—	—	—				N
B3	HPDEF51RP01 a	Bednarik		40	36	30	20	11.72	40	94	2N	
C3	HTPAN18S40RP01 a	Bednarik		—	—	—	—	—				N
D3	HPTTT24S3FP03 a	meissner		333	185	6C5	37	11.89				H ＊
E3	HUVCT01S02RP01 a	HASTING		—	—	—	—	⌒				N
F3	HUVCT01S02RP02 a	HASTING		—	—	—	—	—				N
G3	HUVCT01S02FP01 a	HASTING		⌣	—	—	—	—				N
H3	HUVCT01S03RP01 a	HASTING		⌣	—	—	—	—				N
A4	HUVCT01S03RP02 a	HASTING		15	55	52	29	-12.00				K
B4	HUVCT01S03FP01 a	HASTING		—	—	—	—	⌒				N
27	K a											
28												
29												
30												
31												
32												

Analyzed by: _JMA_   Factura/Blast Analysis: _____

Uploaded by: _JMA_   Folder: _FULL LENGH_

Additional Comments: SCIENTISTS SEQ.   ＊ SUBMIT FOR REDO

Applied
Biosystems

Synthesis Order - 6638 HTPAN08FULLR 362S P02

Run date: 5/19/94
Run ID: 6638 ak
Customer: ANN KIM

P12

1.   jpw
2.
Synthesizer: Synthesizer-2
Model: 394-08
ROM version: 2.00

Sequence name: 6638 HTPAN08FULLR 362S P02
Sequence: CTG CAG TCT CTC TGT GTG G

Cycle: 40 nM CE

End procedure: End CESS
DMT: Off

Comments:
  Sent to "Synthesizer-2" col 3 seq 33 at 5/23/94 9:16 AM.

X

43

ob *Applied*
Biosystems

Synthesis Order - 6639 HTPAN08FULLR 433A P03

Run date: 5/19/94
Run ID: 6639 ak
Customer: ANN KIM

1.   jpw
2.
Synthesizer: Synthesizer-2
Model: 394-08
ROM version: 2.00

Sequence name: 6639 HTPAN08FULLR 433A P03
Sequence: GTA CTT GTC CTC CAT GTG C

Cycle: 40 nM CE

End procedure: End CESS
DMT: Off

Comments:
 Sent to "Synthesizer-2" col 4 seq 34 at 5/23/94 9:18 AM.

abi Applied Biosystems

Synthesis Order - 6640 HTPAN08FULLR 783A P04

P14

Run date: 5/19/94
Run ID: 6640 ak
Customer: ANN KIM

1.   jpw
2.
Synthesizer: Synthesizer-1
Model: 394-08
ROM version: 2.00

Sequence name: 6640 HTPAN08FULLR 783A P03
Sequence: GAA TGC CCA CTC CTT GAT G

Cycle: 40 nM CE

End procedure: End CESS
DMT: Off

Comments:

 Sent to "Synthesizer-1" col 1 seq 31 at 5/23/94 9:19 AM.

45

Human Ge ie Sciences, Inc.   e I.D.(s) _____ _____

Date Initiated: 5/20/94 _____   Results Folder: __05/21/94 38 HGS__

Date Completed: _____   % Good: _____   % Good: _____

Templates	Sequence Reaction	Gel Run
Method:	Method: MANUAL	Machine ID: 38
Prep Person:	Prep Person: DS	Gel Loader: DS
Prep Date:	Prep Date: 5/20/94	Run Date: 5/20/94

#	Sample Name	Scientist name/init	Primer DP/DT	C	A	G	T	Base Spacing	vector	Edited length	# of N's	Trash Code
1-A1	PGEMR lane 3	control	DP	347	191	118	172	9-95		360	5	
2-B1	HTPANO8Rc	ANN KIM	REV	499	276	222	189	10·01	95	340	0	
3-C1	HTPANO8SO4Rc	ANN KIM	REV	303	186	170	158	10·07	95	350	5	
4-D1	HTPANO8S13Rc	ANN KIM	REV	194	69	64	59	10·11	90	420	6	
5-E1	HETAS76Rc	ANN KIM	REV	143	67	118	71	10·03				A CF
6-E1	HETAQ44Rc	ANN KIM	REV	410	198	163	150	10·07	95	350	1	
7-G1	HTHBC32R	HLI	REV	101	63	46	55	10·09	90	420	2	
8-H1	HIBEB91R2	LINSCOR	REV	251	137	110	84	10·00				H
9-A2	HLHBD62R2	LINSCOR	REV	234	208	171	159	10·04	100	270	3	
10-B2	F82A1R	LINSCOR	REV	433	277	160	122	10·06	95	370	1	
11-C2	F81181R	LINSCOR	REV	280	206	106	97	10·03	90	400	0	
12-D2	F811B2R	LINSCOR	REV	124	257	149	137	10·05	95	350	0	
13-E2	F1401R	LINSCOR	REV	423	324	180	184	10·01	95	350	0	
14-F2	F818A1R	LINSCOR	REV	538	215	246	182	10·06	100	410	1	
15-G2	HUVCTO1SO4RA	GAH	REV									no primer
16-H2												no primer
17-A3	PGEMF	control	FOR	306	159	168	152	10·09		360	2	
18-B3	HTPANO8Fc	ANN KIM	FOR	358	155	234	158	10·07				R
19-C3	HTPANO8SO4Fc	ANN KIM	FOR	178	69	152	73	10·07				R
20-D3	HTPANO8SF3Fc	ANN KIM	FOR	121	47	96	69	10·11				AM
21-E3	HETAS76Fc	ANN KIM	FOR	158	95	56	74	10·10	80	370	3	lar
22-F3	HETAQ44Fc	ANN KIM	FOR	246	120	162	112	10·00				F
23-G3	HTHBC32F	HLI	FOR	92	47	52	53	12·00				R
24-H3	F82A1F	LINSCOR	FOR	206	105	146	112	9·96				R
25-A4	F81181F F81181F	LINSCOR	FOR	368	152	277	132	9·76				A
26-B4	F811B2F F811B1F	LINSCOR	FOR	331	137	191	129	10·05	40	320	15	A
27-C4	F1401F	LINSCOR	FOR	477	344	368	222	9·96	40	290	5	
28-D4	F818A1F	LINSCOR	FOR	604	295	299	163	10·00	40	370	4	
29-E4												
30-F4												
31-G4												
32-H4												

Analyzed by: Alice

Uploaded by: HGS   Folder: _____ Scarlet |Full length.

Factura/Blast Analysis: _____

Additional Comments:

Weak signals in lanes 15, 16, 23

- HUVCTO1 SO4RA not enough to Rxn · resubmit

Linscore sample - need to AT least ·5 ul per Rxn - please send proper Amount next time

HLI - only 1 cal please send ·5 ul per RXN

Human Gene Sciences, Inc. Plate I.D.(s ⁄ANUAL DTS_____ _____

Date Initiated:05/20/94 _____

Date Completed: 05/21/94 _____

Results Folder: 05121|GH 35 HGS

% Good: 13/24 % Good: _____

Templates	Sequence Reaction	Gel Run
Method:MISC	Method:BIOMEK/MANUAL	Machine ID: 35
Prep Person:——	Prep Person:TAL	Gel Loader: CDL
Prep Date:——	Prep Date:05/20/94	Run Date: 5120:194

#	Sample Name	Scientist name/init.	Primer DP/DT DT	G	A	T	C	Base Spacing	Vector	Edited length	% Ns	Trash Code
1-A5	PGEMDT	control	DT	53	130	100	79	9.07	40	450	2N	
2-B5	HTPAN08S04RP05	A KIM	5426	188	121	222	69	9.03	40	390	6N	
3-C5	HTPAN08S94RP06	A KIM	5676	170	607	178	72	9.03	40	350	3N	
4-D5	HTPAN08S04RP07	A KIM	5688	210	197	375	62	9.04	40	370	16N	(u)
5-E5	HTPAN08S04RP10	A KIM	6442	155	297	122	54	9.00	100	350	7N	
6-F5	HTPAN08S13RP01	A KIM	685									N
7-G5	HTPAN08S13RP03b	A KIM	5424									N
8-H5	HTPAN08S13RP05	A KIM	5426									N
9-A6	HTPAN08S13RP06	A KIM	5676									N
10-B6	HTPAN08S13RP07	A KIM	5688									N
11-C6	HTPAN08S13RP09	A KIM	6445	91	101	81	37	9.00	40	380	5N	
12-D6	HTPAN08S13RP10	A KIM	6442	12	25	24	36	-12				R
13-E6	HETAS768P01a	A KIM	5809									N
14-F6	HETAS768RP02	A KIM	6152									N
15-G6	HETAQ44RP01	A KIM	5810									N
16-H6	HETAQ44RP02	A KIM	6151									N
17-A7	HARAG42RP01	A. Politis	6575	35	38	29	16	9.00	100	90	4	(H)
18-B7	HTABK03RP04	CRG	6557									N
19-C7	HTABK03FP03	CRG	6558									N
20-D7	HUVCT01S04RP04	GAH	6563	37	113	123	45	9.00	70	320	12N	
21-E7	HUVCT01S04FP05	GAH	6553	250	149	135	105	9.00	40	420	01N	
22-F7	HUVCT01S04FP06	GAH	6554	106	131	192	74	9.00	50	460	11N	
23-G7	HUVCT01S04FP07	GAH	6562	151	231	231	82	9.00	80	320	14N	
24-H7	HE9NG77RP02	GAH	6565	65	74	70	25	9.00	40	300	7N	
25-A8	HE9NG77FP03	GAH	6564	178	129	157	47	9.00	50	375	2N	
26-B8	HE9NG77FP04	GAH	6567	134	120	108	55	9.00	70	370	2N	
27-C8	HE9NG77FP05	GAH	6566	121	158	157	44	9.00	100	375	2N	
28-D8	HFGAN72S04FP02	SOPPET	6358									N
29-E8												
30-F8												
31-G8												
32-H8												

Analyzed by: TCB   Factura/Blast Analysis: _____

Uploaded by: TCB   Folder: Full length Scientist

Additional Comments:

47

Human Gene Sciences, Inc. Plate I.D.(s) _ ANUAL DTS_____

Date Initiated: 5/20/94
Date Completed: 5/21/94

Results Folder: 05/21/94 39 HGS
% Good: 14/32 % Good:

Templates	Sequence Reaction	Gel Run
Method: MISC.	Method: BIOMEK/MANUAL	Machine ID: 39
Prep Person:—	Prep Person: TAL	Gel Loader: CDL
Prep Date:—	Prep Date: 5/20/94	Run Date: 5/20/94

#	Sample Name	Scientist name/init control	Primer DP/DT	Signal Strength G	A	T	C	Base Spacing	% vector	Edited length	% Ns	Trash Code
1-A1	PGEMDT	DT	DT	291	338	213	86	9.87	20	530	2N	
2-B1	HTOAE49RP05	CRG	6585	264	2c5	121	66	9.89	20	400	1N	
3-C1	HTOAE49RP06	CRG	6586	291	191	101	68	9.92	20	380	5N	
4-D1	HPRTK95S01FP04	FISCHER	6129									N
5-E1	HPRTK95S02FP04	FISCHER	6129									
6-F1	HPRTK95S05FP04	FISCHER	6129									
7-G1	HPRTK95S06FP04	FISCHER	6129									
8-H1	HPRTK95S08FP04	FISCHER	6129									
9-A2	HPRTK95S14FP04	FISCHER	6129									
10-B2	HPRTK95S15FP04	FISCHER	6129									
11-C2	HPRTK95S03FP04	FISCHER	6129									
12-D2	HPRTK95S01RP01	FISCHER	5988									
13-E2	HPRTK95S02RP01	FISCHER	5988									
14-F2	HPRTK95S05RP01	FISCHER	5988									
15-G2	HPRTK95S06RP01	FISCHER	5988									
16-H2	HPRTK95S08RP01	FISCHER	5988									
17-A3	HPRTK95S14RP01	FISCHER	5988									
18-B3	HPRTK95S15RP01	FISCHER	5988									
19-C3	HPRTK95S03RP01	FISCHER	5988									
20-D3	HTPAN08RP01b	A KIM	685	262	827	330	721	9.85	130	200	6N	high leuk?
21-E3	HTPAN08RP03b	A KIM	5424	180	200	170	48	9.82	20	290	2N	
22-F3	HTPAN08RP05b	A KIM	5426	294	822	408	1A	9.52	60	220	kN	high luc
23-G3	HTPAN08RP06b	A KIM	5676	190	684	256	91	9.75	60	340	3N	
24-H3	HTPAN08RP07b	A KIM	5688	230	254	349	73	9.52	60	300	4N	
25-A4	HTPAN08S04RP01	A KIM	685	237	344	304	112	9.78	60	300	11N	
26-B4	HTPAN08S04RP03b	A KIM	5424	27	368	502	101	9.77	60	240	3N	0
27-C4	HTPAN08S04RP05	A KIM	5426	243	737	320	89	9.72	60	300	2N	high leg
28-D4	HTPAN08S04RP06	A KIM	5676	212	702	290	110	9.67	68	340	5N	
29-E4	HTPAN08S04RP07	A KIM	5688	250	277	361	84	9.71	60	340	8N	
30-F4	HTPAN08S04RP10	A KIM	6442	191	420	183	77	9.60	60	350	2N	
31-G4	HTPAN08S13RP01	A KIM	685									N
32-H4	HTPAN08S13RP03b	A KIM	5424									N

Analyzed by: _____
Uploaded by: _____ Folder: _____
Additional Comments:

Factura/Blast Analysis: _____

no redos

48

Applied Biosystems

Synthesis Order - 6813 htpan08fp15

Run date: 6/7/94
Run ID: 6813 AMK
Customer: ann kim

1.   KH
2.
Synthesizer: Synthesizer-2
Model: 394-08
ROM version: 2.00

Sequence name: 6813 HTPAN08FP15 - 1520a
Sequence: TAC AGG CAT GTG CCA ACA C

Cycle: 40 nM CE

End procedure: End CESS
DMT: Off

Comments:

Human Genome Sciences, Inc.

Plate I.D.(s) _____ _____

Date Initiated: 05/24/94 _____

Date Completed: 6/9/94 _____

Results Folder: C6/C9/94 27 HGS

% Good: 44% % Good: _____

Templates	Sequence Reaction	Gel Run
Method:	Method: MANUALS	Machine ID: 27
Prep Person:	Prep Person: JSS	Gel Loader: JSS
Prep Date:	Prep Date: 6/08/94	Run Date: 6/8/94

#	Sample Name	Scientist name/init.	Primer DF/DT	Signal Strength C	A	G	T	Base Spacing	vector	Edited length	% N	Trash Code
1-A1	PGEMF	CONTR	FOR	17	21	17	13	-12				R
2-B1	HTPAN08S04Fd	ANN KIM	FOR	141	140	48	66	9.80	45			T
3-C1	HTPAN08S13Fd	ANN KIM	FOR	18	20	17	16	-12				R
4-D1	HTPAN08Fd	ANN KIM	FOR	247	215	125	127	9.85	49			T
5-E1	HE2O142Fb	ANN KIM	FOR	280	231	67	78	9.76	43/78	267	6N	
6-F1	HALSK38F	ANN KIM	FOR	65	280	128	124	9.83	43			M
7-G1	HOSAB71F	ANN KIM	FOR	43	35	19	17	9.85	41			L
8-H1	HE9MF73F	ANN KIM	FOR	311	144	103	144	9.86	44			R/T
9-A2	HPRBMS9S01F	HU	FOR	16	20	15	13	-12				R
10-B2	HPRBMS9S02F	HU	FOR	140	148	41	70	9.87	47			T
11-C2	HPRBMS9S03F	HU	FOR	68	71	23	26	9.81	48			T
12-D2	HPOAA65F	HU	FOR									N
13-E2	HETCN46F	KOVACS	FOR	14	16	15	14	-12				R
14-F2	HNEAA81Fa	HLA	FOR	143	77	52	48	9.84	47			T
15-G2	PGEMR	CONTR	REV	25	20	17	14	-12				R
16-H2	HCACI93R	FISCHER	REV	200	138	40	66	10.00	107	233	3N	
17-A3	HIBECS2R	FISCHER	REV	84	32	24	25	9.83	43			R
18-B3	HETCN46Ra	KOVACS	REV	323	170	63	68	9.91	100	270	4N	
19-C3	HPRBMS9S01R	HU	REV	257	140	72	63	10.08	94	140	4N	
20-D3	HPRBMS9S02R	HU	REV	369	244	81	87	9.96	93			M
21-E3	HPRBMS9S03R	HU	REV	284	209	85	76	10.00	91			M
22-F3	HPOAA6SR	HU	REV									N
23-G3	HTPAN08S04Rd	Ann Kim	REV	290	218	77	64	10.06	97	253	7N	
24-H3	HTPAN08S13Rd	Ann Kim	REV	93	63	35	23	9.92	106	104	Rn/5	
25-A4	HE2O142RB	Ann Kim	REV	438	311	111	114	9.93	95	270	ni	
26-B4	HALSK38R	ANN KIM	REV	447	142	107	133	9.85	95	235	2N	
27-C4	HOSAB71R	ANN KIM	REV	256	193	67	73	9.95	97	150	1N	
28-D4	HE9MF73R	ANN KIM	REV	326	226	81	61	9.80	103	240	9N	
29-E4	HSRDG78aR	REINER	REV	230	167	71	98	9.65	90	194	16N	
30-F4	HSRDG78bR	REINER	REV	312	244	99	97	9.76	92	208	10N	
31-G4	P161C2R	D.Kozak	rev	323	298	101	105	9.98	96	254	2N	
32-H4	P161C3R	D.Kozak	rev	90	51	35	27	9.85	95	205	5N	

Retracked > Julie

Analyzed by: _Julie_ Factura/Blast Analysis: _____

Uploaded by: _Julie_ Folder: Full length + scientist

Additional Comments:

50

Human Genome Sciences, Inc.

Plate I.D.(s) _____ _____

Date Initiated: _____

Date Completed: __06/09/94__

Results Folder: __06/09/94 35 HGS__

% Good: _____ % Good: _____

Templates	Sequence Reaction	Gel Run
Method:	Method: MANUAL	Machine ID: 35
Prep Person:	Prep Person: MICHAEL	Gel Loader: Michael
Prep Date:	Prep Date: 06/08/94	Run Date: ~06/09/94

#	Sample Name	Scientist (name/init)	Primer DP/DT	Signal Strength				Base Spacing	% Vector	Edited Length	% N	Track Code
1-A1	PGEMDT	CONTROL	DT	197	168	113	65	10.19	10	370	2..3	
2-B1	HFGAN72S04CFP04A	soppet/gra	6685	124	130	99	44	10.30	40	300	8..3	
3-C1	HFGAN72S04CRP05A	soppet/gra	6681	117	84	62	84	10.02	60	230	11..3	
4-D1	HETCN46RP01	KOVACS	5458	236	255	174	57	10.24	30	350	4..3	
5-E1	HETCN46RP02	KOVACS	1511	159	187	138	61	10.01	40	360	3..5	
6-F1	HETCN46RP03	KOVACS	6150	134	157	147	63	10.19	30	230	2..3	
7-G1	HETCN46RP04	KOVACS	6632									N
8-H1	HETCN46FP01	KOVACS	6631	80	89	52	27	10.28	50			X
9-A2	HETCN46FP03	KOVACS	1509	74	89	67	36	10.11	5c	350	4..5	
10-B2	HETCN46FP04	KOVACS	1510	133	124	90	46	10.09	30	320	6..3	
11-C2	HTABK03CRP04	CRG	6557									N
12-D2	HTABK03CFP03	CRG	6558									N
13-E2	HSNBL85ARP01	CRG	6694									N
14-F2	HTPAN08S04P12	Ann Kim	6638	265	66	258	97	9.86	30	330	-	
15-G2	HTPAN08S04P13	Ann Kim	6639									N
16-H2	HTPAN08S04P14	Ann Kim	6640	349	263	345	127	10.03	30	320	2..3	
17-A3	HTPAN08S13P12	Ann Kim	6638									N
18-B3	HTPAN08S13P13	Ann Kim	6639									N
19-C3	HTPAN08S13P14	Ann Kim	6670	-								N
20-D3	HE2OI42RP01	Ann Kim	6802	166	248	122	70	9.96	40	310	1..	
21-E3	HE2OI42RP02	Ann Kim	6800									N
22-F3	HALSK38RP02	ANN KIM	5233									N
23-G3	HALSK38RP03	ANN KIM	5513	11	19	67	14	-12.00				R
24-H3	HALSK38RP04	ANN KIM	5677	10	15	59	13	12.00				R
25-A4	HOSAB71RP02	ANN KIM	5233	37	45	35	16	10.34	40	200	11..3	
26-B4	HOSAB71RP03	ANN KIM	5513									N
27-C4	HOSAB71RP04	ANN KIM	5677									N
28-D4	HOSAB71RP05	ANN KIM	5711	161	381	206	52	9.89	40	340	2..3	
29-E4	HOSAB71RP06	ANN KIM	5697									N
30-F4	HE9MF73RP02	ANN KIM	5233									N
31-G4	HE9MF73RP03	ANN KIM	5513									N
32-H4	HE9MF73RP04	ANNKIM	5677									N

Analyzed by: _Michael_

Uploaded by: _Arona_ Folder: _Scientist/follow up_

Factura/Blast Analysis: _____

π More primer peaks, overall weak gel

51

Human Genome Sciences, Inc.

Plate ..D.(s) __manuals__

Date Initiated: __6/10__

Results Folder: __06/11/94 38 HGS__

Date Completed: __6/13__

% Good: _____   % Good: _____

Templates	Sequence Reaction	Gel Run
Method:	Method: MANUAL	Machine ID: 38
Prep Person:	Prep Person: DEBBIE	Gel Loader: ?
Prep Date:	Prep Date: 06/10/94	Run Date: 6/10/94

#	Sample Name	Scientist name/init.	Primer DP/DT	Signal Strength C	A	G	T	Base Spacing	vector	Edited length	% Ns	Trash Code
1-A1	pgemdt	control	dt	115	241	286	216	13.67	20	390	68	
2-B1	HLHCT51PO1'	LINSCOR	PO1	145	290	257	171	13.42	40	400	6.0	
3-C1	VEGF2PF2'	LINSCOR	VEGFx	114	254	195	257	13.39	30	380	9.7	
4-D1	HTPAN08FP15	ANN KIM	6813	74	240	292	343	13.29	30	350	0.6	
5-E1	HTPAN08S04FP15	ANN KIM	6813	98	247	322	322	13.36	30	360	1.1	
6-F1	HTPAN08S13FP15	ANN KIM	6813	32	29	14	53	-12.00				R
7-G1	hhpsi84s13rp02	kinneret	dt	60	128	108	78	13.48	20	200	5.5	
8-H1	hhpsi84s13fp02	kinneret	dt	24	23	19	52	-12.00				R
9-A2	hhpsi84s17rp01	kinneret	dt	46	81	65	67	13.33	30	410	3.9	
10-B2	hhpsi84sestrp04	kinneret	dt	45	56	63	75	13.08	30	410	2.4	
11-C2	hsnme29s27rp01	kinneret	dt	43	35	21	43	-12.00				R
12-D2	hsnme29s27fp02	kinneret	dt									N
13-E2	HCACI93RP20	FISCHER	6815	88	61	66	35	13.43	20	380	4.5	
14-F2	HCACI93FP23	FISCHER	6816	53	116	221	76	13.61	30	410	4.4	
15-G2	HCACI93FP21	FISCHER	6817									N
16-H2	HCACI93FP22	FISCHER	6818									N
17-A3	HIBEC52RP20	FISCHER	6815	46	91	103	77	12.67	30	380	3.2	
18-B3	HIBEC52FP23	FISCHER	6816	29	72	121	63	13.41	20	280	5.4	
19-C3	HIBEC52FP21	FISCHER	6817	32	33	14	37	-12.00				R
20-D3	HIBEC52FP22	FISCHER	6818									N
21-E3	HAEAX59RP01	rad/kincaid	10007	26	30	13	37	-12.00				R
22-F3	HOSBQ33RP01	rad/kincaid	10005									N
23-G3	hhpsh35s14fp15	t curtis	6825	35	54	99	53	12.96	40	250	5.6	
24-H3	hhpsh35s14fp16	t curtis	6826	27	52	54	57	13.11	50	180	5.6	
25-A4	pgemt	control	dpt	613	370	212	207	13.76	60	350	1	
26-B4	HIBEC52501FP	FISCHER		214	129	53	72	13.83	50	350	2	
27-C4	HIBEC52504FP	FISCHER		202	148	53	50	13.83	50	345	1	
28-D4	HIBEC52501FQ	FISCHER		281	165	55	87	13.82	50	345	4	
29-E4	HIBEC52504FQ	FISCHER		230	195	45	69	13.92	50	350	0	
30-F4	m.mr	control	ppR	490	292	251	154	13.90	83	330	1	
31-G4	HTCD25R	RPN	i	256	238	137	99	14.01	92	320	0	
32-H4	iHVEHA21Rb	HLA	t	183	117	81	63	13.75				R

RETRACKED: SRK

Analyzed by: __SRK + IVY__

Factura/Blast Analysis: _____

Uploaded by: __Ivy__   Folder: __Full Length + Scientists__

primer 029
pgem 040

Lot A4C019
A4C018

52

HTPANO8.

PQE60
    5' NCO   1855.   Start

GTA	GCA	CCA	TGG	GAG	GAC	AAG	TAC	TCC

    5' Nco   251   Start

GTA	CGA	CCA	TGG	ATk	ACk	AAG	GAG	AGT

    3' Bam HI   Stop

AGA	TCG	GAT.	CCC	AAC	TAA	AAA	GGC	CCC

PD10.
    5' Bam HI   Start   188
       CGGA

GTA	CGA	GGA	TCCAGGA	GAA	GTA	CTC	CAA

    5' Bam HI   Start   251

GTA	CGA	GGA	TCC	AAT	GAC	GAA	GAG	AGT

    3' Hind III   Stop

CGC	GTA	AAGCTT	GGA	ACT	AAA	AAG	GCT

Synthesis Order - 2240 5' bam hi start 188

Run date: 7/19/94
Run ID: 2240 ak
Customer: ann kim

1.   jpw
2.
Synthesizer: Synthesizer-1
Model: 394-08
ROM version: 2.00

Sequence name: 2240 5' bam hi start 188
Sequence: GTA CGA GGA TCC CAG GAC AAG TAC TCC

Cycle: 40 nM CE

End procedure: End CESS
DMT: Off

Comments:
  Sent to "Synthesizer-1" col 4 seq 34 at 7/19/94 12:13 PM.

Applied Biosystems

Synthesis Order - 2238 3' hind iii stop

Run date: 7/19/94
Run ID: 2238 ak
Customer: ann kim

1.   jpw
2.
Synthesizer: Synthesizer-1
Model: 394-08
ROM version: 2.00

Sequence name: 2238 3' hind iii stop
Sequence: CGC GTA AAG CTT GGA ACT AAA AAG GCC

Cycle: 40 nM CE

End procedure: End CESS
DMT: Off

Comments:
 Sent to "Synthesizer-1" col 2 seq 32 at 7/19/94 12:12 PM.

Applied Biosystems

Synthesis Order - 2239 5'bam hi start 251

Run date: 7/19/94
Run ID: 2239 ak
Customer: ann kim

1.   jpw
2.
Synthesizer: Synthesizer-1
Model: 394-08
ROM version: 2.00

Sequence name: 2239 5'bam hi start 251
Sequence: GTA CGA GGA TCC AAT GAC GAA GAG AGT

Cycle: 40 nM CE

End procedure: End CESS
DMT: Off

Comments:

Sent to "Synthesizer-1" col 3 seq 33 at 7/19/94 12:13 PM.

Synthesis Order - 2241 3' bam hi stop

Run date: 7/19/94
Run ID: 2241
Customer: ann kim

1.   cx
2.
Synthesizer: Synthesizer-2
Model: 394-08
ROM version: 2.00

Sequence name: 3' bam hi stop
Sequence: AGA TCG GAT CCC AAC TAA AAA GGC CCC

Cycle: 40 nM CE

End procedure: End CESS
DMT: Off

Comments:
 Sent to "Synthesizer-2" col 3 seq 33 at 7/20/94 7:10 AM.

ab *Applied Biosystems*

Synthesis Order - 2243 5' nco start 18S

Run date: 7/19/94
Run ID: 2243
Customer: ann kim

1.   cx
2.
Synthesizer: Synthesizer-1
Model: 394-08
ROM version: 2.00

Sequence name: 5'nco start 18S
Sequence: GTA GCA CCA TGG GAG GAC AAG TAC TCC

Cycle: 40 nM CE

End procedure: End CESS
DMT: Off

Comments:
 Sent to "Synthesizer-1" col 1 seq 31 at 7/20/94 11:40 AM.

Applied Biosystems

Synthesis Order - 2244 5' nco start 251

Run date: 7/19/94
Run ID: 2244
Customer: ann kim

1.   cx
2.
Synthesizer: Synthesizer-1
Model: 394-08
ROM version: 2.00

Sequence name: 5' nco start 251
Sequence: GTA CGA CCA TGG ATG ACG AAG GAG AGT

Cycle: 40 nM CE

End procedure: End CESS
DMT: Off

Comments:

Sent to "Synthesizer-1" col 2 seq 32 at 7/20/94 11:41 AM.

Human Genome ~iences, Inc.   Plate I.D.(s ⁷/ FOR 3_REDOS FROM 7/21/94

Date Initiated: 07/22/94
Date Completed: 11/25/91
Results Folder: 11/23/94 50 HGS
% Good: 7/2   % Good:

Templates	Sequence Reaction	Gel Run
Method: MISC	Method: MANUAL/ BIOMEK	Machine ID: 50
Prep Person:	Prep Person: CDL	Gel Loader: FA1
Prep Date:	Prep Date: 07/22/94	Run Date: 7/22/94

#	Sample Name	Scientist name/init.	Primer DP/DT	C	A	G	T	Basel Spacing	vector	Edited length	% Ns	Trash Code
1-A8	BLUESCRIPT	control	DP	487	356	154	143	11.83				m
2-B8	HPOAA6SF	NING	FOR	91	44	44	66	~12.16				R
3-C8	HTOEB44F	SUK	FOR	155	116	45	45	11.41	80	300	.3	
4-D9	HTOEB44AF	SUK	FOR	144	115	45	45	11.88	30	390	0	
5-E9	HTPANO8SO4Fb	A. KIM	FOR	109	199	103	98	11.98	80	270	3	
6-F9	HTPANO8ST3Fb	A. KIM	FOR	272	165	77	7E	11.76	50	340	0	
7-G9	Test PGEMS 1	-	REV	3~2	249	100	114	11.74	40	360	7	
8-H9	2			349	233	145	91	11.58	40			m
9-A10	3			191	113	74	60	11.56	86	184	4	
10-B10	4			310	223	115	81	11.77	92	215	6	
11-C10	5			104	61	41	31	11.71	86	134	5	
12-D10	6			135	104	57	43	11.76	40	140	5	
13-E10												
14-F10												
15-G10												
16-H10												
17-A11												
18-B11												
19-C11												
20-D11												
21-E11												
22-F11												
23-G11												
24-H11												
25-A12												
26-B12												
27-C12												
28-D12												
29-E12												
30-F12												
31-G12												
32-H12												

Analyzed by: THL
loaded by: ✓   Folder: Jill Lincoln, Scient.st
Additional Comments:
- Very small primer peaks
- Gel image looks good

Factura/Blast Analysis:
in comput!

60

Date Initiated: 07/21/94

Date Completed: 7/23/94

Results Folder: 17/23/94 Uc HGS

% Good: _____   % Good: _____

Templates	Sequence Reaction	Gel Run
Method: MISC	Method: BIOMEK/manual	Machine ID: 40
Prep Person: MISC	Prep Person: CDL	Gel Loader: CDL Babu
Prep Date: MISC	Prep Date: 07/22/94	Run Date: 7/22/94

#	Sample Name	Scientist name/init. control	Primer DP/DT	\(C\)	A	G	T	Base Spacing	% vector	Edited length	% N	Trash Code
1-A1	BLUESCRIPT		DP									
2-B1	HPOAA6SR	NING	REV	202	36	208	97	10.07	90	410	3%	
3-C1	HTOEX74R	NING	REV	27	29	23	17	-12.0				B
4-D1	HTPAN08S04Rb	A. KIM	REV	35	42	29	21	9.40				L
5-E1	HTPAN08ST3Rb	A. KIM	REV	83	62	39	31	9.96	100	460	3%	
6-F1	HTOEB44R	SUK	REV	69	49	36	35	10.08	100	350	4%	
7-G1	HTOEB44AR	SUK	REV	78	56	34	30	10.10	100	340	1%	
8-H1	8413E1R	KINNERE	REV	80	58	39	37	10.12	100	370	1%	
9-A2	8413C11R	KINNERE	REV	101	47	46	35	9.43				L
10-B2	8413E2R	KINNERE	REV	81	67	47	31	10.06	90	410	3%	
11-C2	8413E3R	KINNERE	REV	76	30	24	22	9.38	100	380	2%	
D2	8413C12R	KINNERE	REV	44	45	37	24	9.24				L
13-E2	8413C1R	KINNERE	REV	44	32	24	11	9.95	100			L
14-F2	8413E4R	KINNERE	REV	69	58	37	26	10.0	100	400	2%	
15-G2	8413C13R	KINNERE	REV	56	51	33	18	9.95	100	370	2%	
16-H2	8413C2R	KINNERE	REV	67	49	43	21	9.93	100	290	1%	
17-A3	8413C14R	KINNERE	REV	94	76	48	40	9.99	100	320	2%	
18-B3	8413C3R	KINNERE	REV	46	35	30	23	9.31	170	130	1%	
19-C3	8413ESR	KINNERE	REV	80	54	40	29	9.97	100	350	1%	
20-D3	8413E6R	KINNERE	REV	86	71	49	28	9.99	100	390	3%	
21-E3	8413E7R	KINNERE	REV	57	43	40	25	9.25	180	130	2%	
22-F3	8413E8R	KINNERE	REV									N
23-G3	8413C4R	KINNERE	REV	39	35	27	19	9.31	180	310	1%	
24-H3	FB3B1R	LAURIE	REV	74	52	37	29	9.99	100	280	2%	
25-A4	FB17B1R	LAURIE	REV	22	27	21	17	9.49				B
26-B4	FB16C1R	LAURIE	REV									N
27-C4	FB17A1R	LAURIE	REV									N
28-D4	FB18A1R	LAURIE	REV	35	35	24	19	-12.0				B/L
29-E4	FB3C1R	LAURIE	REV	24	22	21	20	9.82				B/L
30-F4	FB16A1R	LAURIE	REV									N
31-G4	FB1C1R	LAURIE	REV	32	27	35	30	9.99	90			B
32-H4	FB19C1R	LAURIE	REV	29	24	24	22	9.87	90			R
				42	34	40	24	-12.0				R

Analyzed by: CDL

Factura/Blast Analysis: _____

Uploaded by: CDL   Folder: sci. seq + fini length

Additional Comments: -Very small primer peaks

61

Applied Biosystems
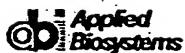
Synthesis Order - 7405 HTPAN08RP20

Run date: 7/25/94
Run ID: 7405 ak
Customer: Ann Kim

1.   jpw
2.
Synthesizer: Synthesizer-2
Model: 394-08
ROM version: 2.00

Sequence name: 7405 HTPAN08RP20   1280S
Sequence: GTG TAT CAC AGT AGT AGC CTC

Cycle: 40 nM CE

End procedure: End CESS
DMT: Off

Comments:

Sent to "Synthesizer-2" col 2 seq 32 at 7/26/94 7:44 AM.

62

ab **Applied**
Biosystems

Synthesis Order - 7406 HTPAN08RP19

Run date: 7/25/94
Run ID: 7406 ak
Customer: Ann Kim

1.   jpw
2.
Synthesizer: Synthesizer-2
Model: 394-08
ROM version: 2.00

Sequence name: 7406 HTPAN08RP19   1031S
Sequence: GCA ATC TGA GTA GAG CAG C

Cycle: 40 nM CE

End procedure: End CESS
DMT: Off

Comments:
    Sent to "Synthesizer-2" col 3 seq 33 at 7/26/94 7:45 AM.

Applied Biosystems

Synthesis Order - 7407 HTPANO8FP18

Run date: 7/25/94
Run ID: 7407 ak
Customer: Ann Kim

1.   jpw
2.
Synthesizer: Synthesizer-2
Model: 394-08
ROM version: 2.00

Sequence name: 7407 HTPANO8FP18   756A
Sequence: GGA ATA GAG TCC ATA TTC TGC

Cycle: 40 nM CE

End procedure: End CESS
DMT: Off

Comments:
  Sent to "Synthesizer-2" col 4 seq 34 at 7/26/94 7:46 AM.

64

Applied Biosystems

Synthesis Order - 7408 HTPAN08FP17

Run date: 7/25/94
Run ID: 7408 ak
Customer: Ann Kim

1.   jpw
2.
Synthesizer: Synthesizer-1
Model: 394-08
ROM version: 2.00

Sequence name: 7408 HTPAN08FP17   561A
Sequence: GAC CAG TTC ACC ATT CCT C

Cycle: 40 nM CE

End procedure: End CESS
DMT: Off

Comments:

  Sent to "Synthesizer-1" col 1 seq 31 at 7/26/94 7:48 AM.

Applied Biosystems

Synthesis Order - 7409 HTPAN08FP16

Run date: 7/25/94
Run ID: 7409 ak
Customer: Ann Kim

1.   jpw
2.
Synthesizer: Synthesizer-1
Model: 394-08
ROM version: 2.00

Sequence name: 7409 HTPAN08FP16   254A
Sequence: CAT ACT CTC TTC GTC ATT GG

Cycle: 40 nM CE

End procedure: End CESS
DMT: Off

Comments:

  Sent to "Synthesizer-1" col 2 seq 32 at 7/26/94 7:49 AM.

Human Genome Sciences, Inc.

Plate ...(s) MISC. DT-2 _____

Date Initiated: 6/2/94 8/1/94 _____

Date Completed: _____

Results Folder: 08/2/94 11 HGS

% Good: 2/8 % Good: _____

Templates	Sequence Reaction	Gel Run
Method:	Method: MANUAL/BIOMEK	Machine ID: 11
Prep Person:	Prep Person: JPF	Gel Loader: JPF
Prep Date:	Prep Date: 8/1/94	Run Date: 8/1/94

G A T C

#	Sample Name	Scientist name/Inits	Primer DP/DT	Signal Strength G	A	T	C	Base Spacing	Vector	Edited length	% N's	Trash Code
1-A5	PGEM	control	DT	197	239	174	97	11.13	20	440	12%	
2-B5	hsnme29s14fp022	kinneret	7442									N
3-C5	hpfbq88testfp01	kinneret	7440	204	222	98	69	11.02	30	360	1%	
4-D5	HTPAN08SO4FPT6	Ann Kim	7409	182	149	97	76	11.08	20	400	4%	
5-E5	HTPAN08SO4FP17	Ann Kim	7408	239	181	166	79	10.99	40	500	1%	
6-F5	HTPAN08SO4FP18	Ann Kim	7407	186	172	68	58	11.22	20	340	1%	
7-G5	HTPAN08SO4RP19	Ann Kim	7406	144	387	136	68	16.97	30	340	1%	
8-H5	HTPAN08SO4RP20	Ann Kim	7405	208	252	80	68	11.14	30	300	4%	
9-A6												
10-B6												
11-C6												
12-D6												
13-E6												
14-F6												
15-G6												
16-H6												
17-A7												
18-B7												
19-C7												
20-D7												
21-E7												
22-F7												
23-G7												
24-H7												
25-A8												
26-B8												
27-C8												
28-D8												
29-E8												
30-F8												
31-G8												
32-H8												

Analyzed by: _____ Factura/Blast Analysis: _____

Uploaded by: _____ Folder: Scout/Full

Additional Comments:)

67

Human Genome Sciences, Inc. Plate I.D.(s) MISC DT_____ _____

Date Initiated: 6/29/94 _____

Date Completed: _08-03-94_____

Results Folder: _08-03-94 11 HGS_____

% Good: _8/31 = 1/270_ % Good: _25 %_

Templates	Sequence Reaction	Gel Run
Method:MISC	Method:BIOMEK/MANUAL	Machine ID: 11
Prep Person:MISC	Prep Person: TES	Gel Loader: TBS
Prep Date:MISC	Prep Date:6/29/94 3'3	Run Date: 7.1

# Sample Name	Scientist name/init.	Primer DP/DT	Signal Strength C	A	G	T	Base Spacing	% vector	Edited length	% N's	Trash Code
1-A1	PGEM	Control	DT	16	175	82	35	-12.00	10	280	6%	lengths
2-B1	HTPAN08S04RP01b	Ann Kim		213	789	117	80	-11.00	10	250	4%	
3-C1	HTPAN08S04RP03b	Ann Kim	5424	218	187	192	45	-12.00	10	340	5%	
4-D1	HTPAN08S04RP05b	Ann Kim	5426	208	494	211	67	-12.00	10	310	/	
5-E1	HTPAN08S04RP06b	Ann Kim	5676	232	580	200	78	-12.00	20	280	4%	
6-F1	HTPAN08S04RP07b	Ann Kim	5688	193	157	231	43	-12.00	50	300	3%	
7-G1	HTPAN08S04RP09b	Ann Kim	6422									N'
8-H1	HTPAN08S04RP10b	Ann Kim	6445	117	184	91	50	-12.00	50	350	3%	
9-A2	HTPAN08S04RP12b	Ann Kim	6838	219	317	165	67	-11.00	10	390	2%	
10-B2	HTPAN08S04RP14b	Ann Kim	6640	302	207	210	92	-12.00	20	340	1%	
11-C2	HTPAN08S04FP15b	Ann Kim	6813	208	163	233	58	-12.00	40	310	/	
12-D2	HSUSH20DS01RP01	Ann Kim	6800									2
13-E2	HSUSH20DS01FP04	Ann Kim	6987									2
14-F2	HSUSH20DS02RP01	Ann Kim	6800									2
15-G2	HSUSH20DS02FP04	Ann Kim	6987									2
16-H2	HSUSH20DS03RP01	Ann Kim	6800									2
17-A3	HSUSH20DS03FP04	Ann Kim	6987									2
18-B3	HSUSH20DS04RP01	Ann Kim	6800									2
19-C3	HSUSH20DS04FP04b	Ann Kim	6987									2
20-D3	HSUSH20DS05RP01b	Ann Kim	6800									2
21-E3	HSUSH20DS05FP04	Ann Kim	6987									2
22-F3	HSUSH20DS06RP01	Ann Kim	6800									2
23-G3	HSUSH20DS06FP04	Ann Kim	6987									2
24-H3	HE2014 2DS01RP01	Ann Kim	6802									2
25-A4	HE2014 2DS01FP03 *	Ann Kim	6986									2
26-B4	HE2014 2DS01RP05	Ann Kim	7027									2
27-C4	HE2014 2DS02RP01	Ann Kim	6802									2
28-D4	HE2014 2DS01FP03 + 50% ot	Ann Kim	6986									2
29-E4	HE2014 2DS02RP05	Ann Kim	7027									2
30-F4	HIBEB69RP01	Ann Kim	7437	126	107	66	67	-12.00	10	440	1%	
31-G4	HIBEB69FP02	Ann Kim	7436									2
32-H4	HPDOM93RP01	Ann Kim	7439	61	73	49	19	-11.00	10	200	3%	langth

Analyzed by: _CYB_ Factura/Blast Analysis: _____

Uploaded by: _LXB_ Folder: _Scientist Full Length_

Additional Comments:

Gel B

68

Human Genome Sciences, Inc.

Plate i.D.(s) _Manual DPs 1_

Date Initiated: 08/02/94 _____

Date Completed: _08|03|94_ _____

Results Folder: _08|03|94 30 HGS_

% Good: _8|33_ % Good: _25%_

Templates	Sequence Reaction	Gel Run
Method:	Method: MANUAL	Machine ID: _30_
Prep Person:	Prep Person: ROX	Gel Loader: _ROX_
Prep Date:	Prep Date: 08/02/94	Run Date: _08|03|94_

#	Sample Name	Scientist name/init	Primer DP/DT	C	A	G	T	Base Spacing	vector	Edited length	% Ns	Trash Code
1-A1	BLUESCRIPT REV	control	ReV	405	263	158	130	10.54	104	200	390	
2-b1	VEG53-HE92	Laurie		13	167	56	49	10.28	97			P
3-C1	HTPANDSS04R1	Ann Kim		114	67	74	65	10.53	96			R
4-D1	HE8BP35S55	Laurie AH		171	74	75	33	-12.00				P
5-E1	HCEOJ49R	soppet/g		59	46	25	25	10.27	107	190	200	
6-F1	HHFBK43R	soppet/g		68	34	43	30	-12.00				P
7-G1	HPRAE77R	soppet/g		62	161	51	52	10.38	98	144	10%	
8-H1	HTEAL83Rc	Kunsch										N
9-A2	HIBEH64S1R	Bednarik		281	204	82	84	10.61	91	209	10%	
10-B2	HIBEH64S2R	Bednarik		258	149	71	71	10.67	94	208	2%	
11-C2	HIBEH64S3R	Bednarik		331	224	149	113	10.19	94	156	20%	
12-D2	HIBEH64S4R	Bednarik		82	65	31	31	10.50	92	200	2%	
13-E2	HIBEH64S5R	Bednarik										N
14-F2	HIBEH64S6R	Bednarik		326	149	53	73	10.60	91	185	10%	
15-G2	HE8BP35S01	GAH		248	80	90	67	10.7				R
16-H2	HE8BP35S05	GAH		202	74	92	68	-12.00				R
17-A3	HE8BP35S06	GAH		140	60	63	39	10.48				R
18-B3	HE8BP35S07	GAH		142	59	61	45	10.73				R
19-C3	HE8BP35S08	GAH		25	100	92	104	-12.00				P
20-D3	HE8BP35S10	GAH		146	54	56	31	10.71				R
21-E3	HE8BP35S13	GAH		204	63	84	65	10.81				R
22-F3	HE8BP35S39	GAH		196	61	62	61	-12.00				P
23-G3	HE8BP35S40	GAH		186	73	74	61	-12.00				P
24-H3	HE8BP35S43	GAH		209	79	65	48	10.93				R
25-A4	HE8BP35S44	GAH		203	73	76	56	10.77				R
26-B4	HE8BP35S45	GAH		70	31	37	29	.0.65				R
27-C4	HE8BP35S46	GAH		154	49	61	44	10.87				R
28-D4	HE8BP35S48	GAH		140	52	59	46	10.90				R
29-E4	HE8BP35S50	GAH		34	31	38	29	-12.00				P
30-F4	HE8BP35S52	GAH		79	35	53	38	10.61				R
31-G4	HE8BP35S53	GAH		78	32	52	38	10.91				P
32-H4	HE8BP35S54	GAH		51	90	34	25	10.10				P

Analyzed by: _ROX_

Uploaded by: _ROX_ Folder: _Sciena Full_

Factura/Blast Analysis: _____

69

Human Genome Sciences, Inc.

Plate I.D.(s) _Manual DPs 2_

Date Initiated: _08/02/94_

Results Folder: _08/03/94 37 HGS_

Date Completed: _08/03/94_

% Good: ~~19/39~~ = % Good: (a,0%)

Templates	Sequence Reaction	Gel Run
Method:	Method: _Manual_	Machine ID: _37_
Prep Person:	Prep Person: _KC X_	Gel Loader: _ROX_
Prep Date:	Prep Date: _08/02/94_	Run Date: _08/02/94_

#	Sample Name	Scientist name/init.	Primer DP/DT	Signal Strength C	A	G	T	Base Spacing	% vector	Edited length	% Ns	Trash Code
1-A5	BLUESCRIPT FOR	CON	FoR	108	70	37	28	1153	10	319	0%	
2-B5	HCEOJ49F	soppet/g		65	70	38	31	11.25	67	200	0%	
3-C5	HHFBK43F	soppet/g		105	61	57	166	-12.00	21	7		D
4-D5	HPRAE77F	soppet/g		221	17	71	49	11.31	81	225	1%	
5-E5	HTPAN08S04Fc	Ann Kim		316	219	108	69	11.30	63	246	0%	
6-F5	HIBEH64S1F	Bednarik		322	216	9	70	11.31	64	263	0%	
7-G5	HIBEH64S2F	Bednarik		573	326	173	133	11.31	61	295	0%	
8-H5	HIBEH64S3F	Bednarik		250	163	86	85	11.33	65	277	0%	
9-A6	HIBEH64S4F	Bednarik		201	145	114	67	11.35	66	271	0%	
10-B6	HIBEH64S5F	Bednarik		301	145	114	67	11.37	66	258	0%	
11-C6	HIBEH64S6F	Bednarik		306	244	121	98	11.38	66	257	0%	
2-D6	HIBEB69Fba	Am Kim		344	172	123	71	11.85				R
13-E6	HTC3H42Faa	Jian N		369	281	131	106	11.34	62	234	0%	
14-F6	H3NAT51Faa	Jian N.	✓	512	256	158	100	11.19	14	300	<0%	
15-G6	HMSB259Faa	Jian N	FCR	716	482	278	162	11.23	61	271	<0%	
16-H6	Bluscript R	control	Rev	48	25	18	78	11.35	101	220	2%	
17-A7	H3NAT51Raa	Jian N.		108	704	279	230	11.30	100	234	0%	
18-B7	HMSB259Raa	Jian N.		116	30	40	35	11.17				R
19-C7	HIBEC52GSi1Ra	Fischer		536	259	134	97	11.12	109	190	30%	
20-D7	HIBEC52GSi2Ra	Fischer		126	53	85	92	-12.00				R
21-E7	HIBEC52GS23Ra	D Kozak		228	163	73	45	11.14	109	214	0%	
22-F7	HIBEC52GS24Ra	D. Kozak										N
23-G7	HE2PD40ARa	D. Kozak		171	131	58	38	11.10	109	189	<0%	
24-H7	HE2PD40B2a	D. Kozak										N
25-A8	LAP34RAa	JPW		63	56	33	28	10.09				R
26-B8	LAP34RBa	JPW										N
27-C8	LAP34RCa	JPW	✓									N
28-D8	HE3MZ50Raa	Brent	Rev	276	69	271	187	-12.00				R
29-E8	Mug's Bluescript F test	control	FoR	303	180	83	92	11.13	110	347	0%	
30-F8												
31-G8												
32-H8												

analyzed by: _ROX_

Uploaded by: _ROX_ Folder: _Scien&Full L_

Factura/Blast Analysis: _____

Additional Comments:

Query= HTPAN08XX
        (1643 letters)

Translating both strands of query sequence in all 6 reading frames

Database: nr
           125,275 sequences; 35,024,229 total letters.
Searching...done

		Reading	High	Smallest Poisson Probability	
Sequences producing High-scoring Segment Pairs:		Frame	Score	P(N)	N
pir|S|A40201	artifact-warning sequence (trans...	+2	241	4.2e-71	3
pir|S|C40201	artifact-warning sequence (trans...	+1	246	2.3e-58	2
pir|S|F40201	artifact-warning sequence (trans...	+2	180	5.5e-21	2
gp|X55777|HSMHCHHS_2	H.sapiens Mahlavu hepatocellular...	+2	190	7.0e-21	1
pir|S|D40201	artifact-warning sequence (trans...	+2	81	2.3e-18	4
gp|L27065|HUMNF2A_1	NF2 gene product [Homo sapiens]	-3	139	1.1e-13	1
pir|S|E40201	artifact-warning sequence (trans...	+1	98	2.5e-13	3
gp|L20321|HUMSTK2A_1	protein serine/threonine kinase ...	-1	137	4.8e-12	1
gp|S58722|S58722_1	X-linked retinopathy protein (3'...	-1	128	1.9e-11	1
pir|S|A46010	X-linked retinopathy protein (C-...	-1	128	1.9e-11	1
gp|M84237|HUMIGTB1A_2	integrin beta-1 subunit [Homo sa...	-3	116	2.5e-10	1
pir|S|A42442	beta 1 integrin subunit, beta 1S...	-3	116	2.5e-10	1
gp|L24521|HUMTRRP_1	transformation-related protein [...	-3	120	2.5e-09	1
gp|U06948|MMU06948_1	Fas ligand [Mus musculus]	+1	84	3.7e-09	2
gp|L11672|HUMKRUPZN_1	zinc finger protein [Homo sapien...	+3	108	1.5e-07	1
gp|U03470|RNU03470_1	ligand for Fas antigen [Rattus n...	+1	84	2.1e-07	2
gp|L26953|HUMPROTXA_1	Homo sapiens chromosomal protein...	+2	101	1.1e-06	1
gp|X14828|CHTNFA_1	Goat mRNA for tumour necrosis fa...	+1	65	6.8e-06	2
pir|S|S06192	tumor necrosis factor alpha prec...	+1	65	6.8e-06	2
gp|A06305|A06305_1	lymphotoxin [None]	+1	99	1.2e-05	1
pir|S|B26359	decay-accelerating factor 2 prec...	-3	96	1.2e-05	1
pir|S|B32877	tumor necrosis factor beta precu...	+1	99	1.4e-05	1
pir|S|S34742	lymphotoxin - human	+1	99	1.4e-05	1
pir|S|S26951	tumor necrosis factor beta - human	+1	99	1.4e-05	1
gp|A00324|A00324_1	tumor necrosis factor beta [Arti...	+1	99	1.4e-05	1
gp|A06316|A06316_1	lymphotoxin [Homo sapiens] >gp|D...	+1	99	1.6e-05	1
gp|D00102|HUMLTX_1	Human lymphotoxin (LT) mRNA, com...	+1	99	1.6e-05	1
gp|Z15026|HSTNFABX_2	lymphotoxin, Tnfb gene product [...	+1	99	1.6e-05	1
gp|X77317|CHTNFAMR_1	tumour necrosis factor alpha [Ca...	+1	63	1.9e-05	2
gp|X55966|OATNFA_1	tumor necrosis factor alpha [Ovi...	+1	67	3.5e-05	2
gp|X55152|OATNFA1_1	tumor necrosis factor alpha (cac...	+1	67	3.5e-05	2
gp|X54859|SSTNFAB_1	Tumour necrosis factor beta [Sus...	+1	95	6.2e-05	1
gp|Z14137|BTNFG_2	tumor necrosis factor alpha [Bos...	+1	65	6.9e-05	2
gp|M12845|RABTNFM_1	Rabbit tumor necrosis factor (TN...	+1	66	7.0e-05	2
gp|M60340|RABTNFB_2	tumor necrosis factor [Oryctolag...	+1	66	7.0e-05	2
gp|M55913|HUMTNFBA_1	tumor necrosis factor-beta [Homo...	+1	93	0.00012	1
pir|S|A26359	decay-accelerating factor 1 prec...	-3	89	0.00015	1
gp|X14800|MMTNFB_3	Murine mRNA 3'-fragment for tumo...	+1	92	0.00015	1
gp|X14800|MMTNFB_1	Murine mRNA 3'-fragment for tumo...	+1	92	0.00017	1
gp|M16819|MUSTNFBA_1	Mouse tumor necrosis factor-beta...	+1	92	0.00017	1

WARNING: Descriptions of 164 database sequences were not reported due to the
          limiting value of parameter V = 40.

71

>gp|U06948|MMU06948_1 ras ligand [Mus musculus]
            Length = 279

  Plus Strand HSPs:

  Score = 84 (40.2 bits), Expect = 0.0029, P = 0.0029
  Identities = 15/34 (44%), Positives = 23/34 (67%), Frame = +1

Query: 529 GHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQ 630
              G + +S +   + G LVI+E G Y++YS+ YFR Q
Sbjct: 165 GTALISGVKYKKGGLVINETGLYFVYSKVYFRGQ 198

  Score = 76 (36.4 bits), Expect = 3.7e-09, Poisson P(2) = 3.7e-09
  Identities = 16/77 (20%), Positives = 36/77 (46%), Frame = +1

Query: 655 NDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVT 834
              N++ +   +Y S   L++   +   +   +S Y G +F L   D ++V+++
Sbjct: 201 NNQPLNHKVYMRNSKYPEDLVLMEEKRLNYCTTGQIWAHSSYLGAVFNLTSADHLYVNIS 260

Query: 835 NEHLIDMDHEASFFGAF 885
              LI+ +   +FFG +
Sbjct: 261 QLSLINFEESKTFFGLY 277

  Score = 40 (19.1 bits), Expect = 0.84, Poisson P(3) = 0.57
  Identities = 6/13 (46%), Positives = 9/13 (69%), Frame = +1

Query: 259 EESMNSPCWQVKW 297
              ++ MN PC Q+ W
Sbjct: 2 QQPMNYPCPQIFW 14

>gp|L11672|HUMKRUPZN_1 zinc finger protein [Homo sapiens] >pir|S|S35305 finger
            protein ZNF91 - human
            Length = 1191

  Plus Strand HSPs:

  Score = 108 (54.9 bits), Expect = 1.5e-07, P = 1.5e-07
  Identities = 20/37 (54%), Positives = 26/37 (70%), Frame = +3

Query: 1371 VQWLTPVIPTFWEPKVGRSRDQEIKTIVTNIVKPHLY 1481
              + +TPVIP WE + G SR QE++TI+ N VKP LY
Sbjct: 1155 IHTITPVIPLLWEAEAGGSRGQEMETILANTVKPLLY 1191

>gp|U03470|RNU03470_1 ligand for Fas antigen [Rattus norvegicus]
            Length = 278

  Plus Strand HSPs:

  Score = 84 (40.2 bits), Expect = 0.0029, P = 0.0029
  Identities = 15/34 (44%), Positives = 23/34 (67%), Frame = +1

Query: 529 GHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQ 630
              G + +S +   + G LVI+E G Y++YS+ YFR Q
Sbjct: 164 GTALISGVKYKKGGLVINEAGLYFVYSKVYFRGQ 197

  Score = 70 (33.5 bits), Expect = 2.1e-07, Poisson P(2) = 2.1e-07
  Identities = 12/39 (30%), Positives = 23/39 (58%), Frame = +1

Query: 769 YSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 885
              +S Y G +F L   D ++V+++   LI+ +   +FFG +
Sbjct: 238 HSSYLGAVFNLTVADHLYVNISQLSLINFEESKTFFGLY 276

EDITED 08/08/94.CON.SEQ Map (1 > 1643)Site and Sequence
Enzymes :   All 417 enzymes (No Filter)
Settings :   Circular, Certain Sites Only, Standard Genetic Code

```
GGCACGAGCGGCTGCCTGGCTGACTTACAGCAGTCAGACTCTGACAGGTTCATGGCTATGATGGAGGTCC
+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+ 70
CCGTGCTCGCCGACGGACCGACTGAATGTCGTCAGTCTGAGACTGTCCAAGTACCGATACTACCTCCAGG

  G  T  S  G  C  L  A  D  L  Q  Q  S  D  S  D  R  F  M  A  M  M  E  V
    A  R  A  A  A  W  L  T  Y  S  S  Q  T  L  T  G  S  W  L  .  W  R  S
  R  H  E  R  L  P  G  .  L  T  A  V  R  L  .  Q  V  H  G  Y  D  G  G  P
+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+
  P  V  L  P  Q  R  A  S  K  C  C  D  S  E  S  L  N  M  A  I  I  S  T  W
   A  R  A  A  A  Q  S  V  .  L  L  .  V  R  V  P  E  H  S  H  H  L  D
    C  S  R  S  G  P  Q  S  V  A  T  L  S  Q  C  T  .  P  .  S  P  P  G

AGGGGGGACCCAGCCTGGGACAGACCTGCGTGCTGATCGTGATCTTCACAGTGCTCCTGCAGTCTCTCTG
+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+ 140
TCCCCCCTGGGTCGGACCCTGTCTGGACGCACGACTAGCACTAGAAGTGTCACGAGGACGTCAGAGAGAC

  Q  G  G  P  S  L  G  Q  T  C  V  L  I  V  I  F  T  V  L  L  Q  S  L  C
    R  G  D  P  A  W  D  R  P  A  C  .  S  .  S  S  Q  C  S  C  S  L  S
   G  G  T  Q  P  G  T  D  L  R  A  D  R  D  L  H  S  A  P  A  V  S  L
+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+
    P  P  G  L  R  P  C  V  Q  T  S  I  T  I  K  V  T  S  R  C  D  R  Q
  L  P  S  G  A  Q  S  L  G  A  H  Q  D  H  D  E  C  H  E  Q  L  R  E  T
    P  P  V  W  G  P  V  S  R  R  A  S  R  S  R  .  L  A  G  A  T  E  R

TGTGGCTGTAACTTACGTGTACTTTACCAACGAGCTGAAGCAGATGCAGGACAAGTACTCCAAAAGTGGC
+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+ 210
ACACCGACATTGAATGCACATGAAATGGTTGCTCGACTTCGTCTACGTCCTGTTCATGAGGTTTTCACCG

  V  A  V  T  Y  V  V  Y  F  T  N  E  L  K  Q  M  Q  D  K  Y  S  K  S  G
  V  W  L  .  L  T  C  T  L  P  T  S  .  S  R  C  R  T  S  T  P  K  V  A
    C  G  C  N  L  R  V  L  Y  Q  R  A  E  A  D  A  G  Q  V  L  Q  K  W
+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+
    T  A  T  V  .  T  Y  K  V  L  S  S  F  C  I  C  S  L  Y  E  L  L  P
   H  S  Y  S  V  H  V  K  G  V  L  Q  L  L  H  L  V  L  V  G  F  T  A
  H  P  Q  L  K  R  T  S  .  W  R  A  S  A  S  A  P  C  T  S  W  F  H  C

ATTGCTTGTTTCTTAAAAGAAGATGACAGTTATTGGGACCCCAATGACGAAGAGAGTATGAACAGCCCCT
+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+ 280
TAACGAACAAAGAATTTTCTTCTACTGTCAATAACCCTGGGGTTACTGCTTCTCTCATACTTGTCGGGGA

  I  A  C  F  L  K  E  D  D  S  Y  W  D  P  N  D  E  E  S  M  N  S  P
    L  L  V  S  .  K  K  M  T  V  I  G  T  P  M  T  K  R  V  .  T  A  P
   H  C  L  F  L  K  R  R  .  Q  L  L  G  P  Q  .  R  R  E  Y  E  Q  P  L
+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+
  M  A  Q  K  K  F  S  S  S  L  .  Q  S  G  L  S  S  S  L  I  F  L  G  Q
    N  S  T  E  .  F  F  I  V  T  I  P  V  G  I  V  F  L  T  H  V  A  G
   Q  K  N  R  L  L  L  H  C  N  N  P  G  W  H  R  L  S  Y  S  C  G  R
```

```
GCTGGCAAGTCAAGTGGCAACTCCGTCAGCTCGTTAGAAAGATGATTTTGAGAACCTCTGAGGAAACCAT
--+---------+---------+---------+---------+---------+---------+--------+  350
CGACCGTTCAGTTCACCGTTGAGGCAGTCGAGCAATCTTTCTACTAAAACTCTTGGAGACTCCTTTGGTA

  C  W  Q  V  K  W  Q  L  R  Q  L  V  R  K  M  I  L  R  T  S  E  E  T  I
   A  G  K  S  S  G  N  S  V  S  S  L  E  R  .  F  .  E  P  L  R  K  P
    L  A  S  Q  V  A  T  P  S  A  R  .  K  D  D  F  E  N  L  .  G  N  H
     Q  C  T  L  H  C  S  R  .  S  T  L  F  I  I  K  L  V  E  S  S  V  M
    A  P  L  D  L  P  L  E  T  L  E  N  S  L  H  N  Q  S  G  R  L  F  G  N
     S  A  L  .  T  A  V  G  D  A  R  .  F  S  S  K  S  F  R  Q  P  F  W

TTCTACAGTTCAAGAAAAGCAACAAAATATTTCTCCCCTAGTGAGAGAAAGAGGTCCTCAGAGAGTAGCA
--+---------+---------+---------+---------+---------+---------+--------+  420
AAGATGTCAAGTTCTTTTCGTTGTTTTATAAAGAGGGGATCACTCTCTTTCTCCAGGAGTCTCTCATCGT

   S  T  V  Q  E  K  Q  Q  N  I  S  P  L  V  R  E  R  G  P  Q  R  V  A
  F  L  Q  F  K  K  S  N  K  I  F  L  P  .  E  K  E  V  L  R  E  .  Q
   F  Y  S  S  R  K  A  T  K  Y  F  S  P  S  E  R  K  R  S  S  E  S  S
    E  V  T  .  S  F  C  C  F  I  E  G  R  T  L  S  L  P  G  .  L  T  A
    R  C  N  L  F  L  L  L  I  N  R  G  .  H  S  F  S  T  R  L  S  Y  C
   K  .  L  E  L  F  A  V  F  Y  K  E  G  L  S  L  F  L  D  E  S  L  L

GCTCACATAACTGGGACCAGAGGAAGAAGCAACACATTGTCTTCTCCAAACTCCAAGAATGAAAAGGCTC
--+---------+---------+---------+---------+---------+---------+--------+  490
CGAGTGTATTGACCCTGGTCTCCTTCTTCGTTGTGTAACAGAAGAGGTTTGAGGTTCTTACTTTTCCGAG

  A  H  I  T  G  T  R  G  R  S  N  T  L  S  S  P  N  S  K  N  E  K  A
   L  T  .  L  G  P  E  E  E  A  T  H  C  L  L  Q  T  P  R  M  K  R  L
  S  S  H  N  W  D  Q  R  K  K  Q  H  I  V  F  S  K  L  Q  E  .  K  G  S
   A  .  M  V  P  V  L  P  L  L  L  V  N  D  E  G  F  E  L  F  S  F  A  R
    S  V  Y  S  P  G  S  S  S  A  V  C  Q  R  R  W  V  G  L  I  F  L  S
     E  C  L  Q  S  W  L  F  F  C  C  M  T  K  E  L  S  W  S  H  F  P  E

TGGGCCGCAAAATAAACTCCTGGGAATCATCAAGGAGTGGGCATTCATTCCTGAGCAACTTGCACTTGAG
--+---------+---------+---------+---------+---------+---------+--------+  560
ACCCGGCGTTTTATTTGAGGACCCTTAGTAGTTCCTCACCCGTAAGTAAGGACTCGTTGAACGTGAACTC

  L  G  R  K  I  N  S  W  E  S  S  R  S  G  H  S  F  L  S  N  L  H  L  R
   W  A  A  K  .  T  P  G  N  H  Q  G  V  G  I  H  S  .  A  T  C  T  .
    G  P  Q  N  K  L  L  G  I  I  K  E  W  A  F  I  P  E  Q  L  A  L  E
     P  R  L  I  F  E  Q  S  D  D  L  L  P  C  E  N  R  L  L  K  C  K  L
    Q  A  A  F  Y  V  G  P  F  .  .  P  T  P  M  .  E  Q  A  V  Q  V  Q  P
     P  G  C  F  L  S  R  P  I  M  L  S  H  A  N  M  G  S  C  S  A  S  S
```

74

```
GAATGGTGAACTGGTCATCCATGAAAAAGGGTTTTACTACATCTATTCCCAAACATACTTTCGATTTCAG
+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+ 630
CTTACCACTTGACCAGTAGGTACTTTTTCCCAAAATGATGTAGATAAGGGTTTGTATGAAAGCTAAAGTC

  N  G  E  L  V  I  H  E  K  G  F  Y  Y  I  Y  S  Q  F  Y  F  R  F  Q
  G  M  V  N  W  S  S  M  K  K  G  F  T  T  S  I  P  K  H  T  F  D  F  R
  E  W  .  T  G  H  P  .  K  R  V  L  L  H  L  F  P  N  I  L  S  I  S
+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+.
  F  P  S  S  T  M  W  S  F  P  N  .  .  M  .  E  W  V  Y  K  R  N  .
   I  T  F  Q  D  D  M  F  F  P  K  V  V  D  I  G  L  C  V  K  S  K  L
  S  H  H  V  P  .  G  H  F  L  T  K  S  C  R  N  G  F  M  S  E  I  E  P

GAGGAAATAAAAGAAAACACAAAGAACGACAAACAAATGGTCCAATATATTTACAAATACACAAGTTATC
+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+ 700
CTCCTTTATTTTCTTTTGTGTTTCTTGCTGTTTGTTTACCAGGTTATATAAATGTTTATGTGTTCAATAG

  E  E  I  K  E  N  T  K  N  D  K  Q  M  V  Q  Y  I  Y  K  Y  T  S  Y
   R  K  .  K  K  T  Q  R  T  T  N  K  W  S  N  I  F  T  N  T  Q  V  I
  G  G  N  K  R  K  H  K  E  R  Q  T  N  G  P  I  Y  L  Q  I  H  K  L  S
+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+.
  S  S  I  F  S  F  V  F  F  S  L  C  I  T  W  Y  I  .  L  Y  V  L  .  G
   L  F  Y  F  F  V  C  L  V  V  F  L  H  D  L  I  N  V  F  V  C  T  I
    P  F  L  L  F  C  L  S  R  C  V  F  P  G  I  Y  K  C  I  C  L  N  D

CTGACCCTATATTGTTGATGAAAAGTGCTAGAAATAGTTGTTGGTCTAAAGATGCAGAATATGGACTCTA
+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+ 770
GACTGGGATATAACAACTACTTTTCACGATCTTTATCAACAACCAGATTTCTACGTCTTATACCTGAGAT

  P  D  P  I  L  L  M  K  S  A  R  N  S  C  W  S  K  D  A  E  Y  G  Y
  L  T  L  Y  C  .  .  K  V  L  E  I  V  V  G  L  K  M  Q  N  M  D  S
   .  P  Y  I  V  D  E  K  C  .  K  .  L  L  V  .  R  C  R  I  W  T  L
+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+.
   .  S  G  I  N  N  I  F  L  A  L  F  L  Q  Q  D  L  S  A  S  Y  P  S  .
   R  V  R  Y  Q  Q  H  F  T  S  S  I  T  T  P  R  F  I  C  F  I  S  E  I
    Q  G  .  I  T  S  S  F  H  .  F  Y  N  N  T  .  L  H  L  I  H  V  R

TTCCATCTATCAAGGGGGAATATTTGAGCTTAAGGAAAATGACAGAATTTTTGTTTCTGTAACAAATGAG
+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+ 840
AAGGTAGATAGTTCCCCCCTTATAAACTCGAATTCCTTTTACTGTCTTAAAAACAAAGACATTGTTTACTC

  S  I  Y  Q  G  G  I  F  E  L  K  E  N  D  R  I  F  V  S  V  N  E
  T  P  S  I  K  G  E  Y  L  S  L  R  K  M  T  E  F  L  F  L  .  Q  M  S
   F  H  L  S  R  G  N  I  .  A  .  G  K  .  Q  N  F  C  F  C  N  K  .
+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+.
   E  M  .  .  P  P  I  N  S  S  L  S  F  S  L  I  K  T  E  T  V  F  S
    G  D  I  L  P  S  Y  K  L  K  L  F  I  V  S  N  K  N  R  Y  C  I  L
   N  W  R  D  L  P  F  I  Q  A  .  P  F  H  C  F  K  Q  K  Q  L  L  H  A
```

EDITED 08/08/94.CON.SEQ Map (1 > 1643)Site and Sequence

```
CACTTGATAGACATGGACCATGAAGCCAGTTTTTTCGGGGCCTTTTTTAGTTGGCTAACTGACCTGGAAAG
+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+   910
GTGAACTATCTGTACCTGGTACTTCGGTCAAAAAAGCCCGGAAAAATCAACCGATTGACTGGACCTTTC

  H  L  I  D  M  D  H  E  A  S  F  F  G  A  F  L  V  G  .  L  T  W  K
     T  .  T  W  T  M  K  P  V  F  S  G  P  F  .  L  A  N  .  P  G  K
  A  L  D  R  H  G  P  .  S  Q  F  F  R  G  L  F  S  W  L  T  D  L  E  R

  C  K  I  S  M  S  W  S  A  L  K  K  P  A  K  K  T  P  .  S  V  Q  F  S
  V  Q  Y  V  H  V  M  F  G  T  K  E  P  G  K  .  N  A  L  Q  G  P  F
     S  S  L  C  P  G  H  L  W  N  K  R  P  R  K  L  Q  S  V  S  R  S  L


AAAAAGCAATAACCTCAAAGTGACTATTCAGTTTTCAGGATGATACACTATGAAGATGTTTCAAAAAATC
+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+   980
TTTTTCGTTATTGGAGTTTCACTGATAAGTCAAAAGTCCTACTATGTGATACTTCTACAAAGTTTTTTAG

  E  K  A  I  T  S  K  .  L  F  S  F  Q  D  D  T  L  .  R  C  F  K  K  S
  K  K  Q  .  P  Q  S  D  Y  S  V  F  R  M  I  H  Y  E  D  V  S  K  N
  K  S  N  N  L  K  V  T  I  Q  F  S  G  .  Y  T  M  K  M  F  Q  K  I

     F  A  I  V  E  F  H  S  N  L  K  .  S  S  V  S  H  L  H  K  L  F  D
  F  F  C  Y  G  .  L  S  .  E  T  K  L  I  I  C  .  S  S  T  E  F  F  R
     F  L  L  L  R  L  T  V  I  .  N  E  P  H  Y  V  I  F  I  N  .  F  I


TGACCAAAACAAACAAACAGAAAACAGAAAACAAAAAAACCTCTATGCAATCTGAGTAGAGCAGCCACAA
+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+   1050
ACTGGTTTTGTTTGTTTGTCTTTTGTCTTTTGTTTTTTTGGAGATACGTTAGACTCATCTCGTCGGTGTT

  D  Q  N  K  Q  T  E  N  R  K  Q  K  N  L  Y  A  I  .  V  E  Q  P  Q
  L  T  K  T  N  K  Q  K  T  E  N  K  K  T  S  M  Q  S  E  .  S  S  H  N
  .  P  K  Q  T  N  R  K  Q  K  T  K  K  P  L  C  N  L  S  R  A  A  T

  S  W  F  L  C  V  S  F  L  F  C  F  F  R  .  A  I  Q  T  S  C  G  C
     V  L  V  F  L  C  F  V  S  F  L  F  V  E  I  C  D  S  Y  L  L  W  L
  Q  G  F  C  V  F  L  F  C  F  V  F  F  G  R  H  L  R  L  L  A  A  V  V


CCAAAAAATTCTACAACACACACTGTTCTGAAAGTGACTCACTTATCCCAAGAAAATGAAATTGCTGAAA
+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+   1120
GGTTTTTTAAGATGTTGTGTGTGACAAGACTTTCACTGAGTGAATAGGGTTCTTTTACTTTAACGACTTT

  P  K  N  S  T  T  H  T  V  L  K  V  T  H  L  S  Q  E  N  E  I  A  E
  Q  K  I  L  Q  H  T  L  F  .  K  .  L  T  Y  P  K  K  M  K  L  L  K
  T  K  K  F  Y  N  T  H  C  S  E  S  D  S  L  I  P  R  K  .  N  C  .  K

  G  F  F  E  V  V  C  V  T  R  F  T  V  .  K  D  W  S  F  S  I  A  S  L
  W  F  I  R  C  C  V  S  N  Q  F  H  S  V  .  G  L  F  I  F  N  S  F
  L  F  N  .  L  V  C  Q  E  S  L  S  E  S  I  G  L  F  H  F  Q  Q  F
```

76

```
     GATCTTTCAGGACTCTACCTCATATCAGTTTGCTAGCAGAAATCTAGAAGACTGTCAGCTTCCAAACATT
     +---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+ 1190
     CTAGAAAGTCCTGAGATGGAGTATAGTCAAACGATCGTCTTTAGATCTTCTGACAGTCGAAGGTTTGTAA

      R  S  F  R  T  L  P  H  I  S  L  L  A  E  I  .  K  T  V  S  F  Q  T  L
       D  L  S  G  L  Y  L  I  S  V  C  .  Q  K  S  R  R  L  S  A  S  K  H
        I  F  Q  D  S  T  S  Y  Q  F  A  S  R  N  L  E  D  C  Q  L  P  N  I
     +---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+
        D  K  L  V  R  G  .  I  L  K  S  A  S  I  .  F  V  T  L  K  W  V  N
       S  R  E  P  S  .  R  M  D  T  Q  .  C  F  D  L  L  S  D  A  E  L  C  .
      I  K  .  S  E  V  E  Y  .  N  A  L  L  F  R  S  S  Q  .  S  G  F  M

     AATGCAATGGTTAACATCTTCTGTCTTTATAATCTACTCCTTGTAAAGACTGTAGAAGAAAGCGCAACAA
     +---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+ 1260
     TTACGTTACCAATTGTAGAAGACAGAAATATTAGATGAGGAACATTTCTGACATCTTCTTTCGCGTTGTT

       M  Q  W  L  T  S  S  V  F  I  I  Y  S  L  .  R  L  .  K  K  A  Q  Q
        .  C  N  G  .  H  L  L  S  L  .  S  T  P  C  K  D  C  R  R  K  R  N  N
         N  A  M  V  N  I  F  C  L  Y  N  L  L  L  V  K  T  V  E  E  S  A  T
     +---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+
        I  C  H  N  V  D  E  T  K  I  I  .  E  K  Y  L  S  Y  F  F  A  C  C
         H  L  P  .  C  R  R  D  K  Y  D  V  G  Q  L  S  Q  L  L  F  R  L  L
      L  A  I  T  L  M  K  Q  R  .  L  R  S  R  T  F  V  T  S  S  L  A  V  I

     TCCATCTCTCAAGTAGTGTATCACAGTAGTAGCCTCCAGGTTTCCTTAAGGGACAACATCCTTAAGTCAA
     +---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+ 1330
     AGGTAGAGAGTTCATCACATAGTGTCATCATCGGAGGTCCAAAGGAATTCCCTGTTGTAGGAATTCAGTT

       S  I  S  Q  V  V  Y  H  S  S  S  L  Q  V  S  L  R  D  N  I  L  K  S
        P  S  L  K  .  C  I  T  V  V  A  S  R  F  P  .  G  T  T  S  L  S  Q
      I  H  L  S  S  S  V  S  Q  .  .  P  P  G  F  L  K  G  Q  H  P  .  V  K
     +---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+
        D  M  E  .  T  T  Y  .  L  L  L  R  W  T  E  K  L  S  L  M  R  L  D  F
         G  D  R  L  Y  H  I  V  T  T  A  E  L  N  G  .  P  V  V  D  K  L  .
          W  R  E  L  L  T  D  C  Y  Y  G  G  P  K  R  L  P  C  C  G  .  T  L

     AAGAGAGAAGAGGCACCACTAAAAGATCGCAGTTTGCCTGGTGCAGTGGCTCACACCTGTAATCCCAACA
     +---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+ 1400
     TTCTCTCTTCTCCGTGGTGATTTTCTAGCGTCAAACGGACCACGTCACCGAGTGTGGACATTAGGGTTGT

        K  E  R  R  G  T  T  K  R  S  Q  F  A  W  C  S  G  S  H  L  .  S  Q  H
         K  R  E  E  A  P  L  K  D  R  S  L  P  G  A  V  A  H  T  C  N  P  N
          R  E  K  R  H  H  .  K  I  A  V  C  L  V  Q  W  L  T  P  V  I  P  T
     +---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+
         S  L  L  P  V  V  L  L  D  C  N  A  Q  H  L  P  E  C  R  Y  D  W  C
        F  L  S  S  A  G  S  F  S  R  L  K  G  P  A  T  A  .  V  Q  L  G  L  M
         L  S  F  L  C  W  .  F  I  A  T  Q  R  T  C  H  S  V  G  T  I  G  V
```

77

```
TTTTGGGAACCCAAGGTGGGTAGATCACGAGATCAAGAGATCAAGACCATAGTGACCAACATAGTGAAAC
+···+···|···+···|···+···|···+···|···+···|···+···|···+···|···+···|···+  1470
AAAACCCTTGGGTTCCACCCATCTAGTGCTCTAGTTCTCTAGTTCTGGTATCACTGGTTGTATCACTTTG

   F  G  N  P  R  W  V  D  H  E  I  K  R  S  R  P  .  .  P  T  .  .  N
 I  L  G  T  Q  G  G  .  I  T  R  S  R  D  Q  D  H  S  D  Q  H  S  E  T
  F  W  E  P  K  V  G  R  S  R  D  Q  E  I  K  T  I  V  T  N  I  V  K
+···+···|···+···|···+···|···+···|···+···|···+···|···+···|···+···|···+
  K  P  F  G  L  H  T  S  .  S  I  L  L  D  L  G  Y  H  G  V  Y  H  F
  K  P  V  W  P  P  Y  I  V  L  D  L  S  .  S  W  L  S  W  C  L  S  V
  N  Q  S  G  L  T  P  L  D  R  S  .  S  I  L  V  M  T  V  L  M  T  F  G

CCCATCTCTACTGAAAGTGCAAAAATTAGCTGGGTGTGTTGGCACATGCCTGTAGTCCCAGCTACTTGAG
+···+···|···+···|···+···|···+···|···+···|···+···|···+···|···+···|···+  1540
GGGTAGAGATGACTTTCACGTTTTTAATCGACCCACACAACCGTGTACGGACATCAGGGTCGATGAACTC

   P  I  S  T  E  S  A  K  I  S  W  V  C  W  H  M  P  V  V  P  A  T  .
   P  S  L  L  K  V  Q  K  L  A  G  C  V  G  T  C  L  .  S  Q  L  L  E
   P  H  L  Y  .  K  C  K  N  .  L  G  V  L  A  H  A  C  S  P  S  Y  L  R
+···+···|···+···|···+···|···+···|···+···|···+···|···+···|···+···|···+
   G  M  E  V  S  L  A  F  I  L  Q  T  H  Q  C  M  G  T  T  G  A  V  Q  S
   G  D  R  S  F  T  C  F  N  A  P  H  T  P  V  H  R  Y  D  W  S  S  S
    W  R  .  Q  F  H  L  F  .  S  P  T  N  A  C  A  Q  L  G  L  .  K  L

AGGCTGAGGCAGGAGAATCGTTTGAACCCGGGAGGCAGAGGTTGCAGTGTGGTGAGATCATGCCACTACA
+···+···|···+···|···+···|···+···|···+···|···+···|···+···|···+···|···+  1610
TCCGACTCCGTCCTCTTAGCAAACTTGGGCCCTCCGTCTCCAACGTCACACCACTCTAGTACGGTGATGT

   E  A  E  A  G  E  S  F  E  P  G  R  Q  R  L  Q  C  G  E  I  M  P  L  H
   R  L  R  Q  E  N  R  L  N  P  G  G  R  G  C  S  V  V  R  S  C  H  Y
    G  .  G  R  R  I  V  .  T  R  E  A  E  V  A  V  W  .  D  H  A  T  T
+···+···|···+···|···+···|···+···|···+···|···+···|···+···|···+···|···+
   A  S  A  P  S  D  N  S  G  P  L  C  L  N  C  H  P  S  I  M  G  S  C
  L  S  L  C  S  F  R  K  F  G  P  P  L  P  Q  L  T  T  L  D  H  W  .  V
   P  Q  P  L  L  I  T  Q  V  R  S  A  S  T  A  T  H  H  S  .  A  V  V

CTCCAGCCTGGCGACAGAGCGAGACTTGGTTTC
+···+···|···+···|···+···|···+··→  1643
GAGGTCGGACCGCTGTCTCGCTCTGAACCAAAG

   S  S  L  A  T  E  R  D  L  V  S
  T  P  A  W  R  Q  S  E  T  W  F
   L  Q  P  G  D  R  A  R  L  G  F
+···+···|···+···|···+···|···+···→
   E  L  R  A  V  S  R  S  K  T  L
   G  A  Q  R  C  L  S  V  Q  N  A
  S  W  G  P  S  L  A  L  S  P  K
```

78

Alignment Report of Untitled, using Clustal method with PAM250 residue weight table.
Monday, August 8, 1994 4:35 PM

Page 1

```
                    10              20              30
     M - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - S T E S M I R   HUVEO91.pep
     M - - - - - - - - - - - - - - - - - - - - - - - - T P P E R L F                   TNFa.pep
1    M - - - - - - - - - - - - - - - - - - - - - - - - T P P E R L F                   TNFb
1    M G A - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - L       LTb
1    M Q Q P V N Y P C P Q I Y W V D S S A T S P W A P P G S V F                       FASL.pep

                    40              50              60
2    - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -           HUVEO91.pep
9    D V E L A E E - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -         TNFa.pep
9    - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -           TNFb
5    G L E G R G G R L Q G R - - - - - - - - - - - - G S L L L A V A G                 LTb
31   S C P S S G P R G P G Q R R P P P P P P P P P S P L P P P S Q                     FASL.pep

                    70              80              90
2    - - - - - - - - - - - - - R R F L S - K V Y S F P M - - -                         HUVEO91.pep
16   - - A L P K K T G G P Q G S R R C L F L S L F S F L I V A G                       TNFa.pep
9    - - L P R V C G T T - - - - - L H L L L L G L L L V - -                           TNFb
26   A T S L V T L - - - - - - - - - - L L A V P I T V L A V L A                       LTb
61   P P P L P P L S P L K K K D N I E L W L P V I F F M V L V A                       FASL.pep

                    100             110             120
14   - - - R K L I L F L V F P V - - - V - - - - - - - - - - -                         HUVEO91.pep
44   - - A T T L F C L L H F G V - - - I G P Q R E E S P R D L S                       TNFa.pep
28   - - - - - - - - L L - - - - - - - P G A Q G L P - G V G                           TNFb
46   L V P Q D Q G - - - - G L V T E T A D P G A Q A Q Q G L G                         LTb
     L V G M G L G M Y Q L F H L Q K E L A E L R E F T N H S L R                       FASL.pep

                    130             140             150
26   - - - - - - - - - R Q T P T Q H F K N Q F - - - - - - - -                         HUVEO91.pep
69   L I S P L A Q A V R S S S R T - - - - P S D K P V A H V V A                       TNFa.pep
40   L T P S A A Q T A R Q H P K M H L A H S T L K P A A H L I G                       TNFb
71   F - - - - Q K L P E E E P E T D L S P G L - - P A A H L I G                       LTb
121  V S S F E K Q I A N P S T P S E T K K P - - R S V A H L T G                       FASL.pep

                    160             170             180
38   - - - - - P - A L H W E H E L G L A F T K N R M N Y T N - K                       HUVEO91.pep
95   N P Q A E G - Q L Q W L N R R A N A L L A N G V E L R D - N                       TNFa.pep
70   D P S K Q N - S L L W R A N T D R A F L Q D G F S L S N - N                       TNFb
95   A P L K - G Q G L G W E T T K E Q A F L T S G T Q F S D A E                       LTb
149  N P R S R S I P L E E W E D T Y G T A L I - S G V K Y K K - G                     FASL.pep

                    190             200             210
61   F L L I P E S G D F I Y S Q V T F R G M T S E C S E I R Q                         HUVEO91.pep
123  Q V V V P S E G L Y L I Y S Q V L F K G Q G C - - - - - -                         TNFa.pep
98   S L L V P T S G I F V Y S Q V V F S G K A Y S P K A - - -                         TNFb
124  G E A L P Q D G L Y Y L Y C L V G Y R G R A P P G G G D P Q                       LTb
177  G L V I N E A G L Y F V Y S K V Y F R G Q S C N S Q P - - -                       FASL.pep
```

```
                    220            230             240
     A G R P N K P D S I T V V I T K V T D S Y P E P T Q - - E L   HUVE091.pep
  _?6 - - - P S T H V L L T H T I S R I A V S Y Q T K V N - - L E   TNFa.pep
  125 - - - P S S P L Y L A H E V Q L F S S Q Y P F H V P - - L D   TNFb
  154 G - - - - R S V T L R S S L Y R A G G A Y G P G T P E L L L   LTb
  204 - - - - - - - - - L S H K V Y M R N F K W P G D L V - - L M   FASL.pep


                    250            260             270
  119 M G T K S V C E - - - - - - - - V G S N W F Q P I Y L G A   HUVE091.pep
  171 S A I K S P C Q R E T P E G - A E A K P W Y E P I Y L G G   TNFa.pep
  150 S S Q K M V Y P - - - - - - - G L Q E P W L H S M Y H G A   TNFb
  180 E G A E T V T P V L D P A R R Q G Y G P L W Y T S V G F G G   LTb
  223 E E K K L N Y - - - - - - C - - T T G Q I W A H S S Y L G A   FASL.pep


                    280            290             300
  140 M F S L Q E G D K L M V N V S D I S L V D Y T K E D K T P F   HUVE091.pep
  199 V F Q L E K G D R L S A E I N R P D Y L D F A E S G Q V Y F   TNFa.pep
  172 A F Q L T Q G D Q L S T H T D G I P H L V L S - P S T V F F   TNFb
  210 L V Q L R R G E R V Y V N I S H P D M V D F A R - G K T E F   LTb
  245 V F N L T V A D H L Y V N I S Q L S L I N F - E E S K T F F   FASL.pep


  170 G A F L L   HUVE091.pep
  229 G I I A L   TNFa.pep
  201 G A F A L   TNFb
  239 G A V M V G   LTb
   '4 G L Y K L   FASL.pep
```

Decoration 'Decoration #1': Box residues that match the Consensus
within 2 distance units.

```
LOCUS        CHTNFAMR_1
DEFINITION   C.hircus TNF-alpha mRNA. Tumour necrosis factor alpha; NCBI
             gi: 452608.
DATE         01-FEB-1994
ACCESSION    X77317
ORGANISM     Capra hircus Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; . .


 to: U06948.Gp_All   check: 3291   from: 1  to: 279

LOCUS        MMU06948_1
DEFINITION   Mus musculus Fas ligand mRNA, complete cds. NCBI gi: 473565.
DATE         29-APR-1994
ACCESSION    U06948
ORGANISM     Mus musculus Eucaryotae; Metazoa; Chordata; Vertebrata;
             Gnathostomata; Mammalia; Eutheria; Rodentia; Myomorpha; Muridae; . .


 Symbol comparison table: Gencoredisk:[Gcgcore.Data.Rundata]Swgappep.Cmp
 CompCheck: 1254


        Gap Weight:   3.000    Average Match:   0.540
     Length Weight:   0.100    Average Mismatch: -0.396


          Quality:    82.2         Length:      160
            Ratio:   0.548           Gaps:        5
 Percent Similarity: 48.993   Percent Identity: 29.530

 X77317.Gp_All x U06948.Gp_All August 9, 1994  17:02  ..


    1 QTLSSSSQASSNKPVAHVVANI.SAPGQLRWGDSYANALKANGVALKDNQ 49
      .. I..I: ... :.III:.:I   I  .  .I I:I.I:.II  :II .I...
  130 ANPSTPSEKKEPRSVAHLTGNPHSRSIPLEWEDTYGTAL.ISGVKYKKGG 178

   50 LVVPNDGLYLIYSQVLFRGHGCPSTPLFLTQTISRIAVSDQTKVNILSAI 99
      II: :.III::II.I.III::I  .  I   I.:.:  .  .  ...:  ::..
  179 LVINETGLYFVYSKVYFRGQSCNNQP..LNHKVYMRNSKYPEDLVLMEEK 226

  100 KSPCHRETPEGAEAKPWYEPIYQGGVFQLEKGDRLSAEINLPEYLDYAES 149
      :  .:       ...:. I  .. I I:II.I.-.:I:I  .:I.  ..::.II
  227 RLNY......CTTGQIWAHSSYLGAVFNLTSADHLYVNISQLSLINFEES 270

  150 GQVYFGIIAL 159
      ..:II:. I
  271 .KTFFGLYKL 279
$
```

LOCUS   MMU06948_1
DEFINITION   Mus musculus Fas ligand mRNA, complete cds. NCBI gi: 473565.
DATE   29-APR-1994
ACCESSION   U06948
ORGANISM   Mus musculus Eucaryotae; Metazoa; Chordata; Vertebrata;
             Gnathostomata; Mammalia; Eutheria; Rodentia; Myomorpha; Muridae; . .

to: X55152.Gp_All check: 8990 from: 1 to: 234

LOCUS   OATNFA1_1
DEFINITION   O.aries mRNA for tumor necrosis factor alpha (TNF-alpha).
             Tumor necrosis factor alpha (cachetin); NCBI gi: 1406.
DATE   09-APR-1992
ACCESSION   X55152
ORGANISM   Ovis aries Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; . . .

Symbol comparison table: Gencoredisk:[Gcgcore.Data.Rundata]Swgappep.Cmp
CompCheck: 1254

            Gap Weight: 3.000   Average Match: 0.540
         Length Weight: 0.100   Average Mismatch: -0.396

               Quality: 109.8   Length: 275
                 Ratio: 0.473   Gaps: 10
     Percent Similarity: 49.321   Percent Identity: 28.054

 U06948.Gp_All x X55152.Gp_All August 9, 1994 17:03 ..

    16 DSSATSSWAPPGSVFPCPSCGPRGPDQRRPPPPPPPVSPLPPPSQPLPLP 65
       ..| ... . ::.|:. ...||.|.   :.
     3 TKSMIRDVELAEEVLSNKAGGPQGSRSCWC.................... 32

    66 PLTPLKKKDHNTNLWLPVVFFMVLVALVGMGLGMYQLFHLQKELAELREF 115
                |.:. |: ||: : .:: |:|:. ::. ||
    33 ...............LSLFSFL....LVAGATTLFCLLHFG.VIGPQRE. 61

   116 TNQSLKVSSFEKQIANP.STPSEKKEPRSVAHLTGNPHSRSIPLEWEDTY 164
       :|| ..||::.:... ...|: .: :.|||:.:| | .:| |:|.|
    62 .EQSPAGPSFNRPLVQTLRSSSQASNNKPVAHVVANI.SAPGQLRWGDSY 109

   165 GTALIS.GVKYKKGGLVINETGLYFVYSKVYFRGQSCNNQP..LNHKVYM 211
       :.||:. ||..|...||: ..|||::||.|.|||::| . | |.|.:. .
   110 ANALMANGVELKDNQLVVPTDGLYLIYSQVLFRGHGCPSTPLFLTHTISR 159

   212 RNSKYPEDLVLMEEKRLNY..'....CTTGQIWAHSSYLGAVFNLTSADHL 255
       . .|....: ::.. :   :   ....:. | .. | |:||.|:..:|:|
   160 IAVSYQTKVNILSAIKSPCHRETLEGAEAKPWYEPIYQGGVFQLEKGDRL 209

   256 YVNISQLSLINFEES.KTFFGLYKL 279
       .:|. ..:::.|| ..:||:. |
   210 SAEINLPEYLDYAESGQVYFGIIAL 234

TRANSLATE of: htpan08xx.dat check: 8776 from: 1 to: 1..3
generated symbols 1 to: 547.
REFORMAT of: Htpan08xx.Dat check: -1 from: 1 to: 1643 August 9, 1994 15:18
(No documentation)

to: U06948.Gp_All check: 3291 from: 1 to: 279

LOCUS   MMU06948_1
DEFINITION   Mus musculus Fas ligand mRNA, complete cds. NCBI gi: 473565.
DATE   29-APR-1994
ACCESSION   U06948
ORGANISM   Mus musculus Eucaryotae; Metazoa; Chordata; Vertebrata;
             Gnathostomata; Mammalia; Eutheria; Rodentia; Myomorpha; Muridae; . .

Symbol comparison table: Gencoredisk:[Gcgcore.Data.Rundata]Swgappep.Cmp
CompCheck: 1254

         Gap Weight: 3.000   Average Match: 0.540
      Length Weight: 0.100   Average Mismatch: -0.396

          Quality: 113.1   Length: 300
            Ratio: 0.427   Gaps: 7
Percent Similarity: 45.276   Percent Identity: 22.047

Htpan08xx.Pep x U06948.Gp_All August 9, 1994 15:29 ..

     9 LQQSDSDRFMAMMEVQGGPSLG.........QTCVLIVIFTVLLQSLCV 48
       :: |....: : .| ..|| | .... : :.. |.|.:
    15 VDSSATSSWAPPGSVFPCPSCGPRGPDQRRPPPPPPPVSPLPPPSQPLPL 64

    49 AVTYVYFTNELKQMQDKYSRSGIACFLKEDDSYWDPNDEESMNSPCWQVK 98
       :.   :| |. ::. . .:. |:   . :|. . :|:
    65 PP....LTPLKKKDHNTNLWLPVVFFMVLV.......ALVGMGLGMYQLF 103

    99 WQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQRVAAHITGTRG 148
       ::|.   . : . .:|..:.. .| |.   .::|..|| ///.:.
   104 HLQKELAELREFTNQSLKVSSFEKQIANPSTPSEKKEPRSVAHLTGNPHS 153

   149 RSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGF 198
       || ..|....:. | .::|.:....:.|:|||:|.|:
   154 RSIPLEWEDT................YGTALISGVKYKKGQLVINETGL 186

   199 YYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTS.YFDPILLMKSARNSC 247
       |::||..||| | :.. |:..: : :||. .| ||:.::||.. |. .:
   187 YFVYSKVYFR......GQSCNNQPLNHKVYMRNSKYPEDLVLMEEKRLNY 230

   248 WSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV 297
       ..:. :: .| | |::|:|...|:::|.:.. ||:::.. .||| : :
   231 CTTGQIWA.HSSYLGAVFNLTSADHLYVNISQLSLINFEESKTFFGLYKL 279

$

TRANSLATE of: htpan08xx.dat check: 8776 from: 1 to: 1643
generated symbols 1 to: 547.
REFORMAT of: Htpan08xx.Dat check: -1 from: 1 to: 1643 August 9, 1994 15:18
(No documentation)

to: X55152.Gp_All check: 8990 from: 1 to: 234

LOCUS   OATNFA1_1
DEFINITION O.aries mRNA for tumor necrosis factor alpha (TNF-alpha).
            Tumor necrosis factor alpha (cachetin); NCBI gi: 1406.
DATE   09-APR-1992
ACCESSION   X55152
ORGANISM   Ovis aries Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; . . .

Symbol comparison table: Gencoredisk:[Gcgcore.Data.Rundata]Swgappep.Cmp
CompCheck: 1254

            Gap Weight: 3.000   Average Match: 0.540
         Length Weight: 0.100   Average Mismatch: -0.396

               Quality: 93.8   Length: 299
                 Ratio: 0.404   Gaps: 9
    Percent Similarity: 47.391   Percent Identity: 22.174

Htpan08xx.Pep x X55152.Gp_All August 9, 1994 15:36 ..

  1 GTSGCLADLQQSDSDRFMAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAV 50
    :|.: : |:: .:.   .: : .|:| :..| : :|..|| :..|.
  2 STKSMIRDVELAEE....VLSNKAGGPQGSRSCWCLSLFSFLL..VAGAT 45

 51 TYVYFTNELKQMQDKYSKSGIACFLKEDDSYWDPNDEESMNSPCWQVKWQ 100
    |..:: :   :: | ...:|:| .:|::.
 46 TLFCLLH........FGVIG............PQREEQSPAGPSFN.... 71

101 LRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQRVAAHITGTRGRS 150
    |.||. .||.|.:.   : .:..||:.:. : .
 72 .RPLVQ..TLRSSSQA.................SNNKPVAHVVANISAP 100

151 NTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFYY 200
    . |...:| ..: ::   ..:.|:::.:||:...|:|.
101 GQLRWGDSYANALMA................NGVELKDNQLVVPTDGLYL 134

201 IYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSK 250
    |||..|| :: ..   .. : .. .|.. .: : :||: :.
135 IYSQVLFRGHGCPSTPLFLTHTISRIAVSYQTKVNILSAIKSPCHRETLE 184

251 DAEYGLY..SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV 297
    :|| : .|||||:|:|...||: ..:. ....:| ...: .: ::..
185 GAEAKPWYEPIYQGGVFQLEKGDRLSAEINLPEYLDYAESGQVYFGIIA 233

TRANSLATE of: htpan08xx.dat check: 8776 from: 1 to: 1643
generated symbols 1 to: 547.
 REFORMAT of: Htpan08xx.Dat check: -1 from: 1 to: 1643 August 9, 1994 15:18
 (No documentation)

 to: X77317.Gp_All check: 8996 from: 1 to: 159

LOCUS   CHTNFAMR_1
DEFINITION C.hircus TNF-alpha mRNA. Tumour necrosis factor alpha; NCBI
           gi: 452608.
DATE   01-FEB-1994
ACCESSION X77317
ORGANISM   Capra hircus Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; . .

 Symbol comparison table: Gencoredisk:[Gcgcore.Data.Rundata]Swgappep.Cmp
 CompCheck: 1254

          Gap Weight: 3.000   Average Match: 0.540
       Length Weight: 0.100   Average Mismatch: -0.396

             Quality: 68.5   Length: 166
               Ratio: 0.466   Gaps: 5
   Percent Similarity: 47.482   Percent Identity: 25.899

 Htpan08xx.Pep x X77317.Gp_All August 9, 1994 15:37 ..

    151 NTL.SSPNSKNEKALGRKINSWESS...RSGHSFLSNLH.....LRNGEL 191
        .|| ||......:|:::: :.. ... |.|.|: ..|. |::.:|
      1 QTLSSSSQASSNKPVAHVVANISAPGQLRWGDSYANALKANGVALKDNQL 50

    192 VIHEKGFYYIYSQTYFR.........FQEEIKENTKNDKQMVQYIYKYT 231
        |:..:.|:|.||||..|| : :.|. . ..|. .|..: ..
     51 VVPNDGLYLIYSQVLFRGHGCPSTPLFLTQTISRIAVSDQTKVNILSAIK 100

    232 SYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEH 281
        | .: |:.. : :|. . ..||||:|:|...||: ...:. ..
    101 S........PCHRETPEGAEAKPWYEPIYQGGVFQLEKGDRLSAEINLPE 142

    282 LIDMDHEASFFGAFLV 297
        .:| ...: .: :::.
    143 YLDYAESGQVYFGIIA 158

$

National Center for Biotechnology Information (NCBI)

Experimental GENINFO(R) BLAST Network Service (Hgssun3)

Wed Aug 10 17:52:09 EDT 1994, Up 16 day(s), 1:44, load: 0.94, 2.16, 3.54

If results of this search are reported or published, please mention that
the computation was performed at the NCBI using the BLAST network service.
Problems with the service should be reported to a local system administrator.

Welcome to the HGS Network Blast Server!

Databases available on the HGS server:

name	description
hgs	HGS/TIGR ESTs human through 08/08/94
hgs_nh	HGS/TIGR non-human ESTs through 08/03/94
thc	TIGR Human Concensus Sequences through 08/08/94
hgs_new	Current Month's HGS/TIGR ESTs through 08/08/94
nt	Non-redundant nucleotide database as of 06/13/94
human-nt	Human sequences from nt database as of 06/13/94
human-est	Human EST sequences from nt database as of 06/13/94
nr	Non-redundant protein database as of 06/13/94
blocks	BLOCKS Motif database, version 7.01

Problems or questions, contact Mike Fannon. Have a BLAST!   -- MRF

BLASTN 1.3.12MP [29-Oct-93] [Build 12:00:00 Nov 11 1993]

Reference: Altschul, Stephen F., Warren Gish, Webb Miller, Eugene W. Myers,
and David J. Lipman (1990). Basic local alignment search tool. J. Mol. Biol.
215:403-410.

Notice: this program is optimized to find nearly identical sequences rapidly.
To identify weak similarities encoded in nucleic acid, use BLASTX or TBLASTN.

Query= HTTCI56R
        (477 letters, both strands)

Database: hgs
        283,367 sequences; 103,639,919 total letters.
Searching...done

| | | High | Smallest Poisson Probability | |
Sequences producing High-scoring Segment Pairs:		Score	P(N)	N
HTTCI56R	Unknown, Group 16833	2277	6.0e-185	1
HTPAN08S04R	Unknown, Group 16833	1437	6.5e-115	1
HTPAN08XX	Unknown, Group 16833	1204	3.1e-93	1
HTPAN08S04FP14	Unknown, Group 16833	1014	7.5e-80	1
HTPAN08S04RP12	Unknown, Group 16833	999	1.2e-78	1
HTPAN08S04RP10	Ligand for Fas antigen [Rattus norvegicus]	751	1.2e-54	1
HTJABC01R	Unknown, Group 16833	629	2.0e-45	1
HETAQ48R	Unknown, Group 16833	640	5.1e-45	1
HT2SE96R	Unknown, Group 16833	116	0.997	1
HLHSM30R	Unknown Sequence	106	1.000000	1
HBNAZ93R	Human adipocyte lipid-binding protein, com...	102	1.000000	1
HPFCO32R	Unknown, Group 10416	99	1.000000	1
HFCAN81R	Unknown, Group 8856	98	1.000000	1
HE2DV72R	Unknown, Group 8856	98	1.000000	1
HE9CT60R	Unknown, Group 8856	98	1.000000	1

HE2PS38R	Unknown, Group 8856	98	1.000000	1
HOSBQ17R	Homo sapiens integral membrane protein, ca...	98	1.000000	1
HE2GB47R	Human calnexin mRNA, complete cds.	98	1.000000	1
HEBCI61R	PBluescript	97	1.000000	1
HE2AY46R	Unknown Sequence	97	1.000000	1
HLT3S32R	Unknown, Group 10589	96	1.000000	1
HE9MG79R	Unknown, Group 41162	96	1.000000	1
HCEOR80R	Unknown, Group 53138	96	1.000000	1
HTBAA86R	Unknown, Group 64	95	1.000000	1
HOSCM10R	Unknown, Group 25755	95	1.000000	1
HFKCA55R	Putative opioid receptor [Homo sapiens]	94	1.000000	1
HAPAU68R	D.discoideum protein-tyrosine kinase-2 (DP...	94	1.000000	1
HPBEJ50R	Unknown, Group 2196	94	1.000000	1
HPBEJ50F	Unknown, Group 2196	94	1.000000	1
HCETB74R	Hardy-Zuckermann 4 feline sarcoma virus (H...	94	1.000000	1
HMEAF90R	Unknown, Group 2196	94	1.000000	1
HE2ED89R	Unknown, Group 38458	93	1.000000	1
HBNAB87R	Unknown, Group 27194	92	1.000000	1
HEBBN20R	Unknown, Group 27194	92	1.000000	1
HLHDP75R	Human mRNA encoding phosphoglycerate kinase.	92	1.000000	1
HT3SF69R	Unknown Sequence	91	1.000000	1
HONAH21R	Unknown, Group 42018	90	1.000000	1
HEPAK86R	ORF [Homo sapiens]	89	1.000000	1
HT2SG40R	Unknown, Group 31877	89	1.000000	1
HE9CU60R	Unknown, Group 8856	89	1.000000	1
HFCAD78R	Unknown, Group 1611	88	1.000000	1
HOSBV50R	Human p62 mRNA, complete cds.	88	1.000000	1
HCEDR10R	Unknown, Group 26335	88	1.000000	1
HT4CL52R	Unknown, Group 49412	88	1.000000	1
HE9CQ82R	H.sapiens mRNA for type I collagen	88	1.000000	1
HE2CT57R	Unknown, Group 8856	87	1.000000	1
HE2AX81R	Unknown, Group 8856	87	1.000000	1
HAUAI83R	Unknown, Group 3372	87	1.000000	1
HCEBF39R	Unknown, Group 10589	87	1.000000	1
HUKAT59F	Unknown, Group 14193	87	1.000000	1

WARNING: Descriptions of 3356 database sequences were not reported due to the
limiting value of parameter V = 50.

>HTTCI56R   Unknown, Group 16833
            Length = 477

  Plus Strand HSPs:

  Score = 2277 (629.2 bits), Expect = 6.0e-185, P = 6.0e-185
  Identities = 465/477 (97%), Positives = 465/477 (97%), Strand = Plus

Query: 1 GGCACGAGGAAGGAAGGGCTTCAGTGACCGGCTGCCTGGCTGACTTACAGCAGTNAGACT 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct: 1 GGCACGAGGAAGGAAGGGCTTCAGTGACCGGCTGCCTGGCTGACTTACAGCAGTNAGACT 60

Query: 61 CTGACAGGATCATGGCTATNATGGAGGTCCAGGGGGGACCCAGCCTGGGACAGACCTGCG 120
             |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Sbjct: 61 CTGACAGGATCATGGCTATNATGGAGGTCCAGGGGGGACCCAGCCTGGGACAGACCTGCG 120

Query: 121 TGCTGATCGTNATCTTCACAGTGCTGCTGCAGTCTCTCTCTGTGTGGCTGTAACTTACGTGT 180
             ||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 121 TGCTGATCGTNATCTTCACAGTGCTGCTGCAGTCTCTCTCTGTGTGGCTGTAACTTACGTGT 180

Query: 181 ACTTTACCAACGAGCTGAAGCAGATGCAGGACAAGTACTCCAAAAGTGGCATTGCTTGTT 240
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 181 ACTTTACCAACGAGCTGAAGCAGATGCAGGACAAGTACTCCAAAAGTGGCATTGCTTGTT 240

```
Query:    252 GATGACAGTTATTGGGACCCCAATGACGAGGAGAGTATGAACAGCCCCTGCTGGCAAGTC 311
              ||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Sbjct:    233 GATGACAGTTATTGGGACCCCAATGACGAAGAGAGTATGAACAGCCCCTGCTGGCAAGTC 292

Query:    312 AAGTGGCAATTCCGTCAGTTCGTTAGAAAGATGGTTTTNAGGACCTCTGAGGNAACCATT 371
              ||||||||| |||||||| ||||||||||||||| ||| || |||||||||| |||||||
Sbjct:    293 AAGTGGCAACTCCGTCAGCTCGTTAGAAAGATGATTTGGAGAACCTCTGAGGAAACCATT 352

Query:    372 TTTACAGTTCAAGNAAGCAACAAATTTTTCTCCCC 406
              | |||||||||||| ||   | || |||| || ||
Sbjct:    353 TCTACAGTTCAAGAAAAGCAACAAATTTTTTCTCC 387

 Score = 490 (135.4 bits), Expect = 9.0e-68, Poisson P(2) = 9.0e-68
 Identities = 102/107 (95%), Positives = 102/107 (95%), Strand = Plus

Query:     26 GACCGGCTGCCTGGCTGACTTACAGCAGTNAGACTCTGACAGGATCATGGCTATNATGGA 85
              || ||||||||||||||||||||||||||| ||||||||||| ||||||||||||| |||||
Sbjct:      6 GAGCGGCTGCCTGGCTGACTTACAGCAGTCAGACTCTGACAGGTTCATGGCTATGATGGA 65

Query:     86 GGTCCAGGGGGGACCCAGCCTGGGACAGACCTGCGTGCTGATCGTNA 132
              |||||||||||||||||||||||||||||||||||||||||||||| |
Sbjct:     66 GGTCCAGGGGGGACCCAGCCTGGGACAGACCTGCGTGCTGATCGTGA 112

 Score = 116 (32.1 bits), Expect = 4.3e-10, Poisson P(3) = 4.3e-10
 Identities = 28/34 (82%), Positives = 28/34 (82%), Strand = Plus

Query:    393 AAATTTTTCTCCCCTAGTGAGGGNAAGNGTTCTT 426
              ||  ||||||||||||||||||| ||| | || |
Sbjct:    376 AATTTTTTCTCCCCTAGTGAGAGAAAGAGGTCCT 409


>HTPAN08S04FP14  Unknown, Group 16833
            Length = 432

 Minus Strand HSPs:

 Score = 1014 (280.2 bits), Expect = 7.5e-80, P = 7.5e-80
 Identities = 206/210 (98%), Positives = 206/210 (98%), Strand = Minus

Query:    313 TTGACTTGCCAGCAGGGGCTGTTCATACTCTCCTCGTCATTGGGGTCCCAATAACTGTCA 254
              | ||||||||||||||||||||||||||||| |||| ||||||||||||||||||||||||
Sbjct:    223 TGGACTTGCCAGCAGGGGCTGTTCATACTCTCTTCGTCATTGGGGTCCCAATAACTGTCA 282

Query:    253 TCTTCTTTTAAGAAACAAGCAATGCCACTTTTGGAGTACTTGTCCTGCATCTGCTTCAGC 194
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:    283 TCTTCTTTTAAGAAACAAGCAATGCCACTTTTGGAGTACTTGTCCTGCATCTGCTTCAGC 342

Query:    193 TCGTTGGTAAAGTACACGTAAGTTACAGCCACACAGAGAGACTGCAGCAGCACTGTGAAG 134
              ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct:    343 TCGTTGGTAAAGTACACGTAAGTTACAGCCACACAGAGAGACTGCAGGAGCACTGTGAAG 402

Query:    133 ATNACGATCAGCACGCAGGTCTGTCCCAGG 104
              || ||||||||||||||||||||||||||||
Sbjct:    403 ATCACGATCAGCACGCAGGTCTGTCCCAGG 432

 Score = 318 (87.9 bits), Expect = 1.1e-39, Poisson P(2) = 1.1e-39
 Identities = 78/96 (81%), Positives = 78/96 (81%), Strand = Minus

Query:    406 GGGGAGAAAAATTTGTTGCTTNCTTGAACTGTAAAAATGGTTNCCTCAGAGGTCCTNAAA 347
              || || | | || |  | ||||||||||| |||||| ||||| |||||||||||| || |||
Sbjct:    129 GGAGAAATATTTTGTTGCTTTTCTTGAACTGTAGAAATGGTTTCCTCAGAGGTTCTCAAA 188

Query:    346 ACCATCTTTCTAACGAACTGACGGAATTGCCACTTG 311
              | |||||||||||||| |||||||| ||||||||||
Sbjct:    189 ATCATCTTTCTAACGAGCTGACGGAGTTGCCACTTG 224
```

88

```
Query:  241 TCTTAAAAGAAGATGACAGTTATTGGGACCCCAATGACGAGGAGAGTATGAACAGCCCCT 300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  241 TCTTAAAAGAAGATGACAGTTATTGGGACCCCAATGACGAGGAGAGTATGAACAGCCCCT 300

Query:  301 GCTGGCAAGTCAAGTGGCAATTCCGTCAGTTCGTTAGAAAGATGGTTTTNAGGACCTCTG 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Sbjct:  301 GCTGGCAAGTCAAGTGGCAATTCCGTCAGTTCGTTAGAAAGATGGTTTTNAGGACCTCTG 360

Query:  361 AGGNAACCATTTTTACAGTTCAAGNAAGCAACAAATTTTTCTCCCCTAGTGAGGGNAAGN 420
            |||| ||||||||||||||||||||| |||||||||||||||||||||||||||||| |||
Sbjct:  361 AGGNAACCATTTTTACAGTTCAAGNAAGCAACAAATTTTTCTCCCCTAGTGAGGGNAAGN 420

Query:  421 GTTCTTAGAGNGTAGGAATTCACNTAATTGGGGCCANGGGAAGAAGCAACANATTGT 477
            |||||||||| |||||||||||| ||||||||||| |||||||||||||| |||||
Sbjct:  421 GTTCTTAGAGNGTAGGAATTCACNTAATTGGGGCCANGGGAAGAAGCAACANATTGT 477


>HTPAN08S04R       Unknown, Group 16833
                Length = 325

  Plus Strand HSPs:

  Score = 1437 (397.1 bits), Expect = 6.5e-115, P = 6.5e-115
  Identities = 301/318 (94%), Positives = 301/318 (94%), Strand = Plus

Query:   56 AGACTCTGACAGGATCATGGCTATNATGGAGGTCCAGGGGGGACCCAGCCTGGGACAGAC 115
            - ||| |||||||||| ||||||||||| ||||||||||||||||||||||||||||||||
Sbjct:    1 AGANTCTGACAGGTTCATGGCTATGATGGAGGTCCAGGGGGGACCCAGCCTGGGACAGAC 60

Query:  116 CTGCGGTGCTGATCGTNATCTTCACAGTGCTGCTGCAGTCTCTCTGTGTGGCTGTAACTTA 175
            |||| ||||||||||| ||||||||||||||||| |||||||||| |||||||||||||||
Sbjct:   61 CTGCTTGCTGATCGTNATCTTCACAGTGCTCCTGCAGTCTCTCTNTGTGTGGCTGTAACTTA 120

Query:  176 CGTGTACTTTACCAACGAGCTGAAGCAGATGCAGGACAAGTACTCCAAAAGTGGCATTGC 235
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  121 CGTGTACTTTACCAACGAGCTGAAGCAGATGCAGGACAAGTACTCCAAAAGTGGCATTGC 180

Query:  236 TTGTTTCTTAAAAGAAGATGACAGTTATTGGGACCCCAATGACGAGGAGAGTATGAACAG 295
            ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Sbjct:  181 TTGTTTCTTAAAAGAAGATGACAGTTATTGGGACCCCAATGACGAAGAGAGTATGAACAG 240

Query:  296 CCCCTGCTGGCAAGTCAAGTGGCAATTCCGTCAGTTCGTTAGAAAGATGGTTTTNAGGAC 355
            ||||||||||||||||||||||||| |||||||| |||||||||||||||| |||| || |
Sbjct:  241 CCCCTGCTGGCAAGTCAAGTGGCAACTCCGTCAGCTCGTTAGAAAGATGATTTTGAGAAC 300

Query:  356 CTCTGAGGNAACCATTTT 373
            |||||||| || | |||
Sbjct:  301 CTCTGAGGGAAACCATTT 318


>HTPAN08XX        Unknown, Group 16833
                Length = 1648

  Plus Strand HSPs:

  Score = 1204 (332.7 bits), Expect = 3.1e-93, P = 3.1e-93
  Identities = 256/275 (93%), Positives = 256/275 (93%), Strand = Plus

Query:  132 ATCTTCACAGTGCTGCTGCAGTCTCTCTGTGTGGCTGTAACTTACGTGTACTTTACCAAC 191
            |||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  113 ATCTTCACAGTGCTCCTGCAGTCTCTCTGTGTGGCTGTAACTTACGTGTACTTTACCAAC 172

Query:  192 GAGCTGAAGCAGATGCAGGACAAGTACTCCAAAAGTGGCATTGCTTGTTTCTTAAAAGAA 251
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  173 GAGCTGAAGCAGATGCAGGACAAGTACTCCAAAAGTGGCATTGCTTGTTTCTTAAAAGAA 232
```

Alignment Report of alignment, using Clustal method with PAM250 residue weight table.
Wednesday, August 10, 1994 2:48 PM

Page 1

```
                    10                  20                  30
        - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -   HUVEO91.pep
   1    - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -   TNFa.pep
   1    - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -   TNFb
   1    - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -   LTb
   1    - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -   FASL.pep
   1    - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -   FAS LIGAND  U06948.pep
   1    G T S G C L A D L Q Q S D S D R F M A M M E V Q G G P S L G   HTPAN08XX.SEQ.FULL.pep
   1    - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -   HUMAN TNF BETA    M55913.pep

                    40                  50                  60
   1    - - - - - - - - - - - - - - - - - - - - - - - - - - - - - M   HUVEO91.pep
   1    - - - - - - - - - - - - - - - - - - - - - - - - - - - - - M   TNFa.pep
   1    - - - - - - - - - - - - - - - - - - - - - - - - - - - - - M   TNFb
   1    - - - - - - - - - - - - - - - - - - - - - - - - - - - - - M   LTb
   1    - - - - - - - - - - - - - - - - - - - - - - - - - - - - - M   FASL.pep
   1    - - - - - - - - - - - - - - - - - - - - - - - - - - - - - M   FAS LIGAND  U06948.pep
  31    Q T C V L I V I F T V L L Q S L C V A V T Y V Y F T N E L K   HTPAN08XX.SEQ.FULL.pep
   1    - - - - - - - - - - - - - - - - - - - - - - - - - - - - - M   HUMAN TNF BETA    M55913.pep

                    70                  80                  90
   2    - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -   HUVEO91.pep
   2    S T E S M I R D V E L - - - - - - - - - - - - - - - - - - -   TNFa.pep
   2    - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -   TNFb
   2    G A L - - - - - - - - - - - - - - - - - - - - - - - - - - -   LTb
   2    Q Q P V N Y P C P Q I - - - - - - - - Y W V - - - - D S S   FASL.pep
   2    Q Q P M N Y P C P Q I - - - - - - - - F W V - - - - D S S   FAS LIGAND  U06948.pep
   1    Q M Q D K Y S K S G I A C F L K E D D S Y W D P N D E E S M   HTPAN08XX.SEQ.FULL.pep
   2    - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -   HUMAN TNF BETA    M55913.pep

                    100                 110                 120
   2    - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -   HUVEO91.pep
  13    - - - - - - - - - - - - - A E E A L P K K T G G P Q G S -   TNFa.pep
   2    - - - - - - T P - - - - - - - P E R L F L P R V C G T T - - -   TNFb
   5    - - - - - - - - - - - - - - - - G L E G R G   LTb
  19    A T S P W A P - - - - - - - P G S V F S C P S L S G P R G P G   FASL.pep
  19    A T S S W A P - - - - - - - P G S V F P C P S C G P R G P D   FAS LIGAND  U06948.pep
  91    N S P C W Q V K W Q L R Q L V R K M I L R T S E E T I S T V   HTPAN08XX.SEQ.FULL.pep
   2    - - - - - T P - - - - - - - P E R L F L P R V C G T T - - -   HUMAN TNF BETA    M55913.pep

                    130                 140                 150
   2    - R R - - - - - - - - - - - - - - - - - - - - - - - - - - -   HUVEO91.pep
  28    - R R C - - - - - - - - - - - - - - - - - - - - - - - - - -   TNFa.pep
  17    - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -   TNFb
  11    G R - - - - - - - - - - - - - - - L Q G - - - - - -   LTb
  42    Q R R P P P P P P P P S P L P P P S Q P P P L P P - - - - -   FASL.pep
  42    Q R R P P P P P P P V S P L P P P S Q P L P L P P - - - - -   FAS LIGAND  U06948.pep
 121    Q E K Q Q N I S P L V R E R G P Q R V A A H I T G T R G R S   HTPAN08XX.SEQ.FULL.pep
  17    - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -   HUMAN TNF BETA    M55913.pep
```

90

```
                         160             170             180
    - - - - - - - - - - - - - - - - - - - - - - - - - - - -   HUVEO91.pep
51  - - - - - - - - - - - - - - - - - - - - - - - - - - - L   TNFa.pep
17  - - - - - - - - - - - - - - - - - - - - - - - - - - - -   TNFb
16  - - - - - - - - - - - - - - - - R G S L L L A V A G A T S  LTb
67  - - - - - - - - - - - - - - - - L S P L K K K D N - I E L  FASL.pep
67  - - - - - - - - - - - - - - - - L T P L K K K D H N T N L  FAS LIGAND  U06948.pep
151 N T L S S P N S K N E K A L G R K I N S W E S S R S G H S F HTPANO8XX.SEQ.FULL.pep
17  - - - - - - - - - - - - - - - - - - - - - - - - - - - -   HUMAN TNF BETA   M55913.pep

                         190             200             210
4   F L S K V Y - S F P M - - - - R K L I L F L V - - F P V - -  HUVEO91.pep
32  F L S - L F - S F L I V A G A T T L F C L L H - - F G V - -  TNFa.pep
17  - L H L L L L G L L L V L - - - - - - - - - - - - - - - - -  TNFb
29  L V T L L L A V P I T V L A V L A L V P Q D Q - - G G L V T  LTb
79  W L P V I F F M V L V A L V G M G L G M Y Q L - - F H L Q K  FASL.pep
80  W L P V V F F M V L V A L V G M G L G M Y Q L - - F H L Q K  FAS LIGAND  U06948.pep
181 L S N L H L R N G E L V I H E K G F Y Y Y S Q T Y F R F Q E  HTPANO8XX.SEQ.FULL.pep
17  - L H L L L L G L L L V L - - - - - - - - - - - - - - - - -  HUMAN TNF BETA   M55913.pep

                         220             230             240
25  - V - - R Q T P T Q H F K N Q F P - - - - - - - - - - - -   HUVEO91.pep
56  - I G P Q R E E S P R D L S L I S P L A Q A V R S S R T P   TNFa.pep
29  - L P G A Q G L P G V G L T P S A A Q T A R Q H P K M H L A  TNFb
57  E T A D P G A Q A Q Q G L G F Q K L P E E E P E T D L S P G  LTb
107 E L A E L R E F T N H S L R V S S F E K Q I A N P S T P S E  FASL.pep
108 E L A E L R E F T N Q S L K V S S F E K Q I A N P S T P S E  FAS LIGAND  U06948.pep
11  E I K E N T K N D K Q M V Q Y I Y K Y T S Y P D P I L L M K  HTPANO8XX.SEQ.FULL.pep
29  - L P G A Q G L P G V G L T P S A A Q T A R Q H P K M H L A  HUMAN TNF BETA   M55913.pep

                         250             260             270
39  - - - - - - - - - - - - - - - - - - - - - - - - - - - -   HUVEO91.pep
85  S D - - K - - - - - - - - - - - - - - - - - - - - - - -   TNFa.pep
58  H S T L K - - - - - - - - - - - - - - - - - - - - - - -   TNFb
87  L - - - - - - - - - - - - - - - - - - - - - - - - - - -   LTb
137 T K K P R - - - - - - - - - - - - - - - - - - - - - - -   FASL.pep
138 K K E P R - - - - - - - - - - - - - - - - - - - - - - -   FAS LIGAND  U06948.pep
241 S A R N S C W S K D A E Y G L Y S I Y Q G G I F E L K E N D HTPANO8XX.SEQ.FULL.pep
58  H S T L K - - - - - - - - - - - - - - - - - - - - - - -   HUMAN TNF BETA   M55913.pep

                         280             290             300
39  - - - - - - - - - - - - - - - - - - - - - - - - A L H W   HUVEO91.pep
88  - - - - - - P V A H V V A N P Q A E G - - - - - - Q L Q W   TNFa.pep
63  - - - - - - P A A H L I G D P S K Q N - - - - - - S L L W   TNFb
88  - - - - - - P A A H L I G A P L K - G - - - - - - Q G L G W  LTb
142 - - - - - - S V A H L T G N P R S R S - - - - - - I P L E W  FASL.pep
143 - - - - - - S V A H L T G N P H S R S - - - - - - I P L E W  FAS LIGAND  U06948.pep
271 R I F V S V T N E H L I D M D H E A S F F G A F L V G L T W  HTPANO8XX.SEQ.FULL.pep
63  - - - - - - P A A H L I G D P S K Q N - - - - - - S L L W   HUMAN TNF BETA   M55913.pep
```

91

```
                    310             320             330
  3  E H E L G L A - - - -F T K N R M N -Y T N K -F L L I P E   HUVE091.pep
105  L N R R A N A - - - -L L A N G V E -L R D N -Q L V V P S   TNFa.pep
 80  R A N T D R A - - - -F L Q D G F S -L S N N -S L L V P T   TNFb
105  E T T K E Q A - - - -F L T S G T Q -F S D A E G L A L P Q  LTb
160  E D T Y G T A - - - - -L I S G V K -Y K K G -G L V I N E  FASL.pep
161  E D T Y G T A - - - - -L I S G V K -Y K K G -G L V I N E  FAS LIGAND  U06948.pep
301  K E K A I T S K L F S F Q D D T L R C F K K S D Q N K Q T E  HTPAN08XX.SEQ.FULL.pep
 80  R A N T D R A - - - -F L Q D G F S -L S N N -S L L V P T   HUMAN TNF BETA    M55913.pep


                    340             350             360
 67  S - - - -G D Y F I Y S Q V T F R G M T S E C - - - -S E I  HUVE091.pep
129  E - - - -G L Y L I Y S Q V L F K G Q - -G C - - - - - - -   TNFa.pep
104  S - - - -G I Y F V Y S Q V V F S G K A Y S - - - - - - - -  TNFb
130  D - - - -G L Y Y L Y C L V G Y R G R A P P G - - - -G G -   LTb
183  A - - - -G L Y V Y S K V Y F R G Q S C N - - - - - - - -   FASL.pep
184  T - - - -G L Y F V S K V Y F R G Q S C N - - - - - - - -   FAS LIGAND  U06948.pep
331  N R K Q K N L Y A I V E Q P Q P K N S T T H T V L K V T H L  HTPAN08XX.SEQ.FULL.pep
104  S - - - -G I Y F V Y S Q V V F S G K A Y S - - - - - - - -  HUMAN TNF BETA    M55913.pep


                    370             380             390
 89  R Q A G R P N K P D S - -I T V V I T K V T D S - - - - - -   HUVE091.pep
146  - - - - - -P S T H V L - -L T H T I S R I A V S - - - - - -  TNFa.pep
122  - -P K A P S S P L Y - -L A H E V Q L F S S Q - - - - - -   TNFb
151  - - -D P Q G R S V T - -L R S S L Y R A G G A - - - - - -   LTb
201  - - S Q P - - - - - - -L S H K V Y M R N F K - - - - - -   FASL.pep
202  - - N Q P - - - - - - -L N H K V Y M R N S K - - - - - -   FAS LIGAND  U06948.pep
 61  S Q E N E I A E R S F R T L P H I S L L A E I K T V S F Q T  HTPAN08XX.SEQ.FULL.pep
122  - -P K A P S S P L Y - -L A H E V Q L F S S Q - - - - - -   HUMAN TNF BETA    M55913.pep


                    400             410             420
111  - - - - - - - - - - - -Y P E P T Q - -L L M G T K S V C E  HUVE091.pep
163  - - - - - - - - - - - -Y Q T K V N - -L L S A I K S P C Q  TNFa.pep
142  - - - - - - - - - - - -Y P F H V P - -L L S S Q K M V Y P   TNFb
170  - - - - - - - - - - - -Y G P G T P E L L L E G A E T V T P  LTb
215  - - - - - - - - - - - -Y P G D L V - -L M E E K K L N Y C  FASL.pep
216  - - - - - - - - - - - -Y P E D L V - -L M E E K R L N Y C  FAS LIGAND  U06948.pep
391  L M Q W L T S S V F I I Y S L R L K K A Q Q S I S Q V V Y H  HTPAN08XX.SEQ.FULL.pep
142  - - - - - - - - - - - -Y P F H V P - -L L S S Q K M V Y P   HUMAN TNF BETA    M55913.pep


                    430             440             450
127  V G S - - - - - - - - - - -N - - - - - - - - - - - -W F   HUVE091.pep
179  R E T - - - - - - - - - - P E - - G A E A K P - - -W Y   TNFa.pep
158  - - - - - - - - - - - - - - - - G L Q E P - - -W L   TNFb
188  V L D - - - - - - - - - - - P A R R Q G Y G P L - - -W Y  LTb
231  - - - - - - - - - - - - - - - -T T G Q I - - -W A   FASL.pep
232  - - - - - - - - - - - - - - - -T T G Q I - - -W A   FAS LIGAND  U06948.pep
421  S S S L Q V S L R D N I L K S K E R R G T T K R S Q F A W C  HTPAN08XX.SEQ.FULL.pep
158  - - - - - - - - - - - - - - -G L Q E P - - -W L   HUMAN TNF BETA    M55913.pep
```

Alignment Report of alignment, using Clustal method with PAM250 residue weight table.
Wednesday, August 10, 1994 2:48 PM

Page 4

```
                    460               470               480
 33  Q P I Y L G A M F S L Q E - - - - - - - - - - - G D K L M   HUVE091.pep
192  E P I Y L G G V F Q L E K - - - - - - - - - - - G D R L S   TNFa.pep
165  H S M Y H G A A F Q L T Q - - - - - - - - - - - G D Q L S   TNFb
203  T S V G F G G L V Q L R R - - - - - - - - - - - G E R V Y   LTb
238  H S S Y L G A V F N L T V - - - - - - - - - - - A D H L Y   FASL.pep
239  H S S Y L G A V F N L T S - - - - - - - - - - - A D H L Y   FAS LIGAND  U06948.pep
451  S G S H L S Q H F G N P R W V D H E I K R S R P P T N P I S HTPAN08XX.SEQ.FULL.pep
165  H S M Y H G A A F Q L T Q - - - - - - - - - - - G D Q L S   HUMAN TNF BETA    M55913.pep

                    490               500               510
151  V N V S D I S L V D Y - - - - - - - - - - T K E D K T F - - -  HUVE091.pep
210  A E I N R P D Y L D F - - - - - - - - - - A E S G Q V Y - - -  TNFa.pep
183  T H T D G I P H L V L - - - - - - - - - - S - P S T V F - - -  TNFb
221  V N I S H P D M V D F - - - - - - - - - - A R - G K T F - - -  LTb
256  V N I S Q L S L I N F - - - - - - - - - - E - E S K T F - - -  FASL.pep
257  V N I S Q L S L I N F - - - - - - - - - - E - E S K T F - - -  FAS LIGAND  U06948.pep
481  T E S A K I S W V C W H M P V V P A T E A E A G E S F E P G  HTPAN08XX.SEQ.FULL.pep
183  T H T D G I P H L V L - - - - - - - - - - S - P S T V F - - -  HUMAN TNF BETA    M55913.pep

                    520               530
169  - - - - - F G A F L - - - - - - - - - - - L       HUVE091.pep
228  - - - - - F G I I A - - - - - - - - - - - L       TNFa.pep
200  - - - - - F G A F A - - - - - - - - - - - L       TNFb
238  - - - - - F G A V M - - - - - - - - - - V G       LTb
273  - - - - - F G L Y K - - - - - - - - - - - L       FASL.pep
274  - - - - - F G L Y K - - - - - - - - - - - L       FAS LIGAND  U06948.pep
 11  R Q R L Q C G E I M P L H S S L A T E R D L V     HTPAN08XX.SEQ.FULL.pep
200  - - - - - F G A F A - - - - - - - - - - - L       HUMAN TNF BETA    M55913.pep
```

Decoration 'Decoration #1': Box residues that match the Consensus within 2 distance units.

Human Genome ~iences, Inc.　　　Pla、 .D.(s) _____ ____

Date Initiated: _____　　Results Folder: _O8/10/94_ _22_ _HGS_

)ate Completed: _58·10·94_ _____　% Good: _____　% Good: _____

Templates	Sequence Reaction	Gel Run
Method:	Method: MANUAL	Machine ID: **22**
Prep Person:	Prep Person: ACS	Gel Loader: ALw
Prep Date:	Prep Date: 08/0**9**/94	Run Date: **08/09/94**

# 1-A9	Sample Name	Scientist name/init	Primer DP/DT	C	A	G	T	Base Spacing	vector	Edited length	%Ns	Trash Code
	R luseript									AAN-OFF GEL		
2-B9	HLMACO64RP02	NING/HL	7196									N
3-C9	HLMACO67RP02	NING/HL	7196									N
4-D9	HLMACO68RP02	NING/HL	7196									N
5-E9	HPDOM93RP01 ✓	ANN KIM	7439	373	296	153	117	-12.00				P
6-F9	HPDOM93FP02 X	ANN KIM	7479	269	187	114	73	11.06				D
7-G9	HIBEB69RP01 ✓	ANN KIM	7437	128	144	65	83	10.74	40	360		
8-H9	HIBEB69FP02 ✗	ANN KIM	7436									N
9-A10	HTPAN08S04FP17 ✓	ANN KIM	7408	460	329	252	156	-12.00				P
10-B10	HTPAN08S04FP18 ✓	ANN KIM	7407	443	306	252	147	-12.00				R
11-C10	HTPAN08S04RP19 ✓	ANN KIM	7406	51	78	53	41	-12.00				P
12-D10	HTPAN08S04RP20 ✓	ANN KIM	7405	683	856	249	252	10.27	20	330		
3-E10	HE9MF73S05RP16 ✓	ANN KIM	7098	167	218	98	64	10.41	32	330		
14-F10	HE9MF73S05FP17 ✓	ANN KIM	7105	248	219	172	91	10.38	30	330		
15-G10	HE9MF73S05RP18 ✓	ANN KIM	7106	212	319	140	117	10.41	30	380		
16-H10	HE9MF73S05RP19	ANN KIM	7109	206	377	111	115	10.43	20	400		
17-A11	HE9MF73S05FP20 ✓	ANN KIM	7128	211	207	134	77	10.46				P
18-B11	HE9MF73S05RP21 ✓	ANN KIM	7170	272	354	127	190	10.35	50	350		
19-C11	HE9MF73S05FP22 ✓	ANN KIM	7171	359	293	290	153	10.46	40	390		
20-D11	HE20142RP01 ✓	ANN KIM	6802	307	314	130	112	10.43	10	390		
21-E11	HE20142FP03 ✓	ANN KIM	6986	275	172	111	81	10.32				P
22-F11	HE20142RP05 ✓	ANN KIM	7027	337	332	143	95	10.33	20	400		
23-G11	HETAS76RP02 λ	ANN KIM	6152									N
24-H11	HETAS76RP03 ✓	ANN KIM	7112	278	226	91	110	10.41	20	400		
25-A12	HCEOJ23S30AP02	D.KOZAK	1989	78	48	27	27	10.43	20	400		
26-B12	HCEOJ23S30BP02	D.KOZAK	1989									N
27-C12	HCEOJ23S30CP02	D.KOZAK	1989	68	42	23	23	10.61	20	390		
28-D12	HCEOJ23S30DP02	D.KOZAK	1989	116	62	37	41	10.17	50	391		
29-E12	HCEOJ23S30EP02	D.KOZAK	1989	102	63	35	36	10.46	20	420		
30-F12	HCEOJ23S30FP02	D.KOZAK	1989	46	68	37	38	10.43	20	400		
31-G12	HCEOJ23S30GP02	D.KOZAK	1989	115	73	39	36	10.58	20	430		
32-H12	HCEOJ23S30HP02	D.KOZAK	1989	88	54	20	25	10.55	20	391		

`nalyzed by: _Dm_
ploaded by: _Jm_　Folder: _SCI_/_FL_
Additional Comments:
19~4/150c @ 13:19

Factura/Blast Analysis: _____

Human Genome Sciences, Inc.

Plate I.D.(s) _____ _____

Date Initiated: _____

Date Completed: _____

Results Folder: 08/10/94 38 HGS

% Good: _____ % Good: _____

Templates	Sequence Reaction	Gel Run
Method:	Method:	Machine ID: 38
Prep Person:	Prep Person:	Gel Loader: Karen
Prep Date:	Prep Date:	Run Date: 8/9

#	Sample Name	Scientist name/init. control	Primer DP/DT for	Signal Strength C	A	G	T	Base Spacing	Vector	Edited Length	% Ns	Trash Code
1	bluescriptF			318	30	54	123	0.03		580		
2	HPRCU93F	Politis		240	158	98	84	10.57	50	200	1	—
3	HTPAN08S04F	A. Kim		283	190	136	115	10.58	50	250	1	—
4	HIBEB69F	A. Kim		145	74	77	57	10.46	20	200	1	—
5	HPDDM93F	A. Kim		59	37	29	28	10.47	20	240	3	—
6	HETAS76F	A. Kim		205	92	112	81	10.47	50	350	1	—
7	HTOAS71Fa	HLA		351	279	119	67	10.53	50	350	1	
8	HFSBC6533F1	Hudson										
9	HFSBC6533F2	Hudson							50			T
10	HFSBC6533F3	Hudson							50			R
11	HE2PD40AF	D. Kozak										I
12	HILCJ44AF	D. Kozak		128	82	42	39	10.54	50	400	1	—
13	HE2CB95AF	D. Kozak		176	117	68	50	10.63	50	340	1	—
14	bluescript HCEOJ23S30KR	Control	rev									R
15	HT2SA16Ra	RPW										R
16	HCEOJ23S30AR	D.Kozak		106	62	48	37	10.65	95	305	1	—
17	HCEOJ23S30BR	D.Kozak										R
18	HCEOJ23S30CR	D.Kozak		338	196	99	70	10.70	100	450	1	—
19	HCEOJ23S30DR	D.Kozak										N
20	HCEOJ23S30ER	D.Kozak										R
21	HCEOJ23S30FR	D.Kozak										R
22	HCEOJ23S30GR	D.Kozak		228	109	65	55	10.69	100	370	1	—
23	HCEOJ23S30HR	D.Kozak		150	92	56	45	10.69	100	360	1	—
24	HCEOJ23S30IR	D.Kozak		213	146	58	64	10.72	100	340	2	—
25	HCEOJ23S30JR	D.Kozak		100	54	39	38	10.76	95	350	1	—
26	HCEOJ23S30KR bluescript	D.Kozak	B/S	164	101	63	48	10.69	95	360	1	—
27	HCEOJ23S30LR	D.Kozak							98	430		.
28	HCEOJ23S30MR	D.Kozak		109	59	38	32	10.70	100	150		
29	HCEOJ23S30NR	D.Kozak		231	119	68	45	10.74	100	380	1	—
30	HCEOJ23S30OR	D.Kozak		211	108	68	49	10.69	100	360	1	—
31	HCEOJ23S30PR	D.Kozak										R
32	HPRCU93Ra	Politis		495	228	132	105	10.74	100	300	1	—

alyzed by: Kin

uploaded by: Kin Folder: Pt/Sci

Factura/Blast Analysis: _____

Additional Comments:

Buffer leak   gel problem

95

Human Genome Sciences, Inc.

Plate I.D.(s) _____ _____

Date Initiated: _____

Date Completed: _____

Results Folder: 08|10|94 39 HCS

% Good: _____ % Good: _____

Templates	Sequence Reaction	Gel Run
Method:	Method:	Machine ID: 39
Prep Person:	Prep Person:	Gel Loader: Karen
Prep Date:	Prep Date:	Run Date: 8/9

#	Sample Name	Scientist name/init	Primer DP/DT	Signal Strength C	A	G	T	Base Spacing	vector	Edited length	% N's	Trash Code
1-A1	HTPANO8S04R B/S	A KIM	rev	303	418	158	211	10.57		330	3	-
2-B1	HIBEB69R	A KIM		588	26	112	100	10.76	100	330	1	-
3-C1	HPDDM93R	A KIM		266	305	170	39	10.43	100	310	1	-
4-D1	HETAS76R	A KIM		454	307	158	103	10.52	95	290	1	-
5-E1	HFSBC6533R1	Hudson							95			R
6-F1	HFSBC6533R2	Hudson		179	166	105	56	10.53	95	305	1	-
7-G1	HFSBC6533R3	Hudson		194	183	75	60	10.58	95	250	4	
8-H1	HSRDG78R1c	a chopra		391	321	129	127	10.47	90	340	3	-
9-A2	HSRDG78R1d	a chopra		204	349	141	135	10.52	90	360	2	-
10-B2	HSJAF39R1c	a chopra		458	381	164	130	10.49	95	230	2	-
11-C2	HSJAF39R1d	a chopra		690	505	214	203	10.44	95	340	2	-
2-D2	HGBBH79R1c	a chopra	(	236	196	78	81	10.56	95	350	2	-
13-E2	HGBBH79R1d	a chopra		148	116	63	61	10.54	95	380	2	-
14-F2	DNAE02+346R	FISCHER										N
15-G2	DNASE04+346R	FISCHER										N
16-H2	BLUESCRIPTr HTPANO8S04R	control										R
17-A3												
18-B3												
19-C3												
20-D3												
21-E3												
22-F3												
23-G3												
24-H3												
25-A4												
26-B4												
27-C4												
28-D4												
29-E4												
30-F4												
31-G4												
32-H4												

Kim upload to FL/Sci

96

Human Genome Sciences, Inc.

Plate I.D.(s) _____ _____ ✓

Templates	Sequence Reaction	Gel Run
Method:	Method: manual	Machine ID: 14
Prep Person:	Prep Person: karen	Gel Loader: Andrew
Prep Date:	Prep Date: 8/10/94	Run Date: 8/10/94

#	Sample Name	Scientist name/unit control	Primer DP/DT FOR	Signal Strength C	A	G	T	Base Spacing	Vector	Edited Length	% Ns	Trash Code
1	bluescriptF		FOR	264	155	64	118	10.90		380		
2	HE2S10F	A KIM	FOR	75	3	17	25	10.22	30	200	2	-
3	HE2S11F	A KIM	FOR	346	72	116	71	10.77	45	280	2	-
4	HE2S12F	A KIM	FOR	202	166	131	56	10.16	40	120	2	
5	HE2S13F	A KIM	FOR	315	257	93	77	10.70	40	270	2	
6	HE2S14F	A KIM	FOR	234	186	163	53	10.54	40	270	1	-
7	HE2S15F	A KIM	FOR	264	254	93	92	10.54	40	280	1	-
8	HE2S16F	A KIM	FOR					10.61	40	260	2	-
9	HE2S17F	A KIM	FOR									N
10	HE2S18F	A KIM	FOR	446	335	125	121	10.75	40	330	1	N
11	HE2S19F	A KIM	FOR	340	312	130	143	10.85	40	300	1	-
12	HE2S20F	A KIM	FOR	322	411	156	154	10.69	40	510	1	-
13	HE2S21F	A KIM	FOR	218	208	149	122	10.52	40	230	2	-
14	HE2S22F	A KIM	FOR	403	316	167	45	10.41	45	250	2	-
15	HE2S23F	A KIM	FOR	597	45	140	177	10.56	40	280	2	-
16	HE2S24F	A KIM	FOR	474	434	118	124	10.56	60	300	2	-
17	HE2S25F	A KIM	FOR	615	367	151	126	10.76	50	300	2	-
18	HE2S26F	A KIM	FOR	436	333	123	110	10.59	50	300	3	-
19	HE2S27F	A KIM	FOR	606	325	111	114	10.59	50	300	3	-
20	HE2S28F	A KIM	FOR					10.73	50	300	2	-
21	HE2OI42F	A KIM	FOR	457	250	148	124	10.61	40	320	2	R
22	HSUSH20F	A KIM	FOR	273	301	123	116	10.62	50	300	2	-
23	HI8EB69F	A KIM	FOR	313	146	84	51	10.52	20	370	<1	-
24	HPDDM93F	A KIM	FOR	443	354	100	110	10.54	35	325	2	-
25	HE9MF73S05F	A KIM	FOR	571	252	100	116	10.61	50	300	2	-
26	HE9MF73S07F	A KIM	FOR	454	314	114	109	10.49	50	275	2	-
27	HTPAN08S04F	A KIM	FOR	552	423	162	149	10.49	45	325	2	-
28	HTPAN08S13F	A KIM	FOR	613	40	158	46	10.49	40	350	2	-
29	HTPAN08F	A KIM	FOR	732	449	147	132	10.51	40	300	1	-
30	HALSK38F	A KIM	FOR	194	51	204	157	10.52	40	270	1	-
31	HOSAB71F	A KIM	FOR	554	417	174	84	10.53	45	280	2	-
32	HE9MF73F	A KIM	FOR	443	460	138	125	10.41	50	280	2	-

attacked - IVY

alyzed by: Kim

uploaded by: Kim   Folder: F.L/Sci

Factura/Blast Analysis: _____

Additional Comments:
all looks good.
Strong primers

all samples - 11, 12, 13F all had
5F break ~85 bp

97

Human Genome Sciences, Inc.

Plate I.D.(s) ___manuals___

Date Initiated: _____

Date Completed: ___8/11/94___

Results Folder: ___08/11/94 18 HGS___

% Good: __24/32__ % Good: _____

Templates	Sequence Reaction	Gel Run
Method:	Method: manual	Machine ID: _18_
Prep Person:	Prep Person: karen	Gel Loader: _Kn_
Prep Date:	Prep Date: 8/10/94	Run Date: _8·10_

#	Sample Name		Scientist name/init control	Primer DP/DT rev	Signal Strength C	A	G	T	Base Spacing	Vector	Edited Length	% N's	Trash Code
1	bluescriptR				200	121	76	68	9.99	101	349	2.9	
2	HE2S10R	X	A KIM	REV									2
3	HE2S11R	✓	A KIM	REV	258	131	98	81	10.06	99	331	1.5	
4	HE2S12R	✓	A KIM	REV	161	98	65	49	10.04	101	339	1.8	
5	HE2S13R	✓	A KIM	REV	249	141	84	68	10.06	96	364	3.6	
6	HE2S14R	✓	A KIM	REV	171	98	58	46	10.04	101	349	4.0	
7	HE2S15R	✓✓	A KIM	REV	215	159	82	65	10.05	101	349	1.7	
8	HE2S16R	X	A KIM	REV									2
9	HE2S17R	X	A KIM	REV									2
10	HE2S18R	✓	A KIM	REV	273	212	124	106	10.00	100	—		I
11	HE2S19R	✓	A KIM	REV	309	206	163	91	10.03	101	—		I
12	HE2S20R	✓	A KIM	REV	383	225	118	101	10.04	101	—		I
13	HE2S21R	✓	A KIM	REV	34	238	128	109	9.95	100	320	1.6	
14	HE2S22R	✓	A KIM	REV	476	228	137	115	9.92	101	319	2.2	
15	HE2S23R	✓	A KIM	REV	369	270	141	119	9.95	99	261	4.9	
16	HE2S24R	✓	A KIM	REV	404	255	126	111	9.91	101	319	1.6	
17	HE2S25R	✓	A KIM	REV	29	187	116	96	10.02	100	290	1.0	
18	HE2S26R	✓	A KIM	REV	322	218	130	110	10.00	100	330	1.5	
19	HE2S27R	✓	A KIM	REV	310	203	126	101	9.98	100	330	4.8	
20	HE2S28R	X MIXED	A KIM	REV	237	170	106	80	9.82	100	—		I
21	HE2O142R	✓	A KIM	REV	176	122	74	61	9.95	101	408	9.9	
22	HSUSH2OR	✓	A KIM	REV	197	123	74	59	10.00	101	319	1.6	
23	HIBEB69R	v.small signal	A KIM	REV									2
24	HPDOM93R	✓	A KIM	REV	274	182	104	86	9.93	100	330	0.6	
25	HE9MF73S05R	✓	A KIM	REV	159	115	70	72	10.11	99	371	7.9	
26	HE9MF73S07R	✓	A KIM	REV	197	117	63	62	10.02	101	369	7.4	
27	HTPAN08S04R	✓	A KIM	REV	363	246	135	118	10.07	101	349	2.3	
28	HTPAN08S13R	✓	A KIM	REV	229	140	94	68	10.08	95	315	1.3	
29	HTPAN08R	✓	A KIM	REV	567	360	155	183	9.99	101	269	0.7	
30	HALSK38R	✓	A KIM	REV	297	350	58	57	9.96	95	345	1.2	
31	HOSAB71R	✓	A KIM	REV	393	320	157	117	9.99	102	348	3.7	
32	HE9MF73R	✓	A KIM	REV	503	418	214	152	10.02	96	334	0.6	

serviced - IVY

Analyzed by: ___IVY___

Uploaded by: ___IVY___ Folder: ___Full length + scientists___ Factura/Blast Analysis: _____

Additional Comments:

98

Human Genome Sciences, Inc.

Plate I.D.(s) __manuals 2__

Date Initiated: _____

Date Completed: __8-18-94__

Results Folder: __08/18/94__   __40 HGS__

% Good: _____   % Good: _____

Templates	Sequence Reaction	Gel Run
Method: MISC.	Method: MANUAL/BIOMEK	Machine ID: 40
Prep Person: MISC.	Prep Person: SMR	Gel Loader: ASP
Prep Date: MISC.	Prep Date: 08/17/94	Run Date: 08/17/94

#	Sample Name	Scientist name/init.	Primer DP/DT	Signal Strength C	A	G	T	Base Spacing	% vector	Edited length	% N#	Trash Code
1-A5	bluescript	control	REV	258	149	104	87	10.10	~20	370	4N/11	
2-B5	HHPSI21R	soppet/g	rev									N
3-C5	HPRAE75R	soppet/g	rev	439	326	147	130	10.07	92	358	7N/16	
4-D5	HMNAD13CR	ANN KIM	rev	103	65	37	31	9.90	100	141	3N/14	
5-E5	HMNAD13DR	ANN KIM	rev	219	135	66	48	10.02	95	305	4N/16	
6-F5	HTPBY11CR	ANN KIM	rev	63	48	31	32	9.81	103	210	11N/56	
7-G5	HPTBY11DR HTPBY11DR	ANN KIM	rev	79	63	33	35	9.79	100	230	4N/56	
8-H5	HLTBR89AR	ANN KIM	rev	543	338	145	148	10.02	97	369	4N/27	
9-A6	HLTBR89BR	ANN KIM	rev	423	299	166	121	10.01	96	336	1N/31	
10-B6	HLTBA03AR	ANN KIM	rev	462	382	198	182	9.95	97	359	4N/16	
11-C6	HLTBA03BR	ANN KIM	rev	380	372	174	155	9.76	95	345	3N/31	
2-D6	HSUDK13AR HCSDK	ANN KIM	rev	498	331	191	162	9.87	99	341	5N/16	
13-E6	HSUDK13BR HCSDK	ANN KIM	rev	596	374	236	213	9.92	94	349	7N/31	
14-F6	HTTCI56AR	ANN KIM	rev	510	378	190	151	9.83	100	260	3N/16	
15-G6	HTTCI56BR	ANN KIM	rev	238	225	102	71	9.88	100	300	2N/31	
16-H6	HMSBZ43AR	ANN KIM	rev	524	405	230	199	9.91	94	321	100N/56	
17-A7	HMSBZ43BR	ANN KIM	rev	480	361	215	191	9.92	103	303	4N/31	
18-B7	HE2FF12R	D.Kozak	revers	258	217	100	86	9.87	97	310	5N/11	
19-C7	HAFAD33AR	D.Kozak	revers	156	123	171	47	9.89	96	342	1N/31	
20-D7	HAFAD33BR	D.Kozak	revers	28	103	52	46	9.93				P, R
21-E7 ✓	HE6CL09Rdmso	MING	REV	204	185	116	102	9.75	97			
22-F7 ✓	HE6CL68Rdmso	MING	REV	190	133	92	82	7.79			n	
23-G7 ✓	HE6CL96Rdmso	MING	REV	206	130	87	80	9.86	99			M
24-H7	PSK SP6	control	SP6	135	107	110	79	-12				R
25-A8	TTS - AT	PFY		103	96	119	47	9.91		380	2%	
26-B8	TTS - BT			81	47	96	35	9.95		340	3%	
27-C8	TTS - CT			85	110	102	48	10.09		440	1%	
28-D8	P - ETR 015			15	87	68	27	10.03				u
29-E8												
30-F8												
31-G8												
32-H8												

Analyzed by: __DND/JSS__

loaded by: __ASP__   Folder: __Full length + scientists__

Factura/Blast Analysis: _____

Additional Comments: __Retracked-JS__
   __✓ = SFS__

99

Human Genome Sciences, Inc.

Plate I.D.(s) _manuals   1_

Date Initiated: _____

Date Completed: **8118194**

Results Folder: _05/18/94 35 HGS_

% Good: _____   % Good: **88°/**

Templates	Sequence Reaction	Gel Run
Method:MISC	Method:BIOMEK/MANUAL	Machine ID: 35
Prep Person:MISC	Prep Person: SMR	Gel Loader: ASP
Prep Date:MISC	Prep Date: 8/17/94	Run Date: 8/17/94

#	Sample Name	Scientist name/init	Primer DF/DT	Signal Strength C	A	G	T	Base Spacing	vector	Edited length	% N	Trash Code
1-A1	bluescript	control	for	361	222	162	134	10.19	~40	410	>1	
2-B1	HPFDL91Fa	jian Ni	for	81	56	42	30	9.95	~50	350	>1	
3-C1	HUNAE76Fa	jian Ni	for	58	37	34	28	10.04				T
4-D1	HE9CF32Fa	jian Ni	for	41	40	29	21	10.00				I
5-E1	HE8AS10Fa	jian Ni	for	79	42	44	42	9.99	~70			T
6-F1	HHPSI21F	soppet/g	for									N
7-G1	HPRAE75F	soppet/g	for	206	136	66	97	9.86	50	350	>1	
8-H1	HMNAD13CF	ANN KIM	for	130	81	41	57	9.91	50	330	>1	
9-A2	HMNAD13DF	ANN KIM	for	152	284	172	129	10.07	50	330	1.5	
10-B2	HTPBY11CF	ANN KIM	for	97	72	40	30	9.80	50	350	>1	
11-C2	HPTBY11BF HT?B4115F	ANN KIM	for	110	76	46	34	9.78	50	310	>1	
12-D2	HLTBR89AF	ANN KIM	for	428	374	199	120	9.80	50	370	>1	
13-E2	HLTBR89BF	ANN KIM	for	508	317	215	125	9.81	50	400	>1	
14-F2	HLTBA03AF	ANN KIM	for	394	362	272	198	9.81	40	590	0	
15-G2	HSUDK13AF HCSDK	ANN KIM	for	346	368	148	146	9.80	50	400	>1	
16-H2	HLTBA03BF	ANN KIM	for	279	326	88	116	9.83	50	370	>1	
17-A3	HSUDK13BF HCRDK	ANN KIM	for	508	358	256	132	9.81	50	400	1.2	
18-B3	HTTCI56AF	ANN KIM	for	457	312	159	97	9.73	50	360	3.0	
19-C3	HTTCI56BF	ANN KIM	for	220	200	81	55	9.71	40	400	1.5	
20-D3	HMS8Z43AF	ANN KIM	for	420	379	201	111	9.76	40	290	4.1	
21-E3	HMS8Z43BF	ANN KIM	for	738	4N	273	164	9.80	50	390	>1	
22-F3	CNB8PG2	KOVACS	for	60	44	32	23	9.79	~60	230	1.7	
23-G3	CNB8PG3	KOVACS	for	257	218	81	88	9.88	~10	470	>1	
24-H3	CNB8PG4	KOVACS	for	338	365	110	145	9.75	~20	300	3.6	
25-A4	CNB8PG5	KOVACS	for	208	179	152	95	9.83	~50	400	2.5	
26-B4	CNB8PG6	KOVACS	for	348	220	43	119	9.79	~70	360	1.9	
27-C4	CNB8PG7	KOVACS	for	465	203	161	145	9.81	~90	350	>1	
28-D4	CNB8PG8	KOVACS	for	328	198	154	119	9.79	~10	500	>1	
29-E4	bluescript	control	rev	269	217	104	89	9.84	95	300	>1	
30-F4	LAP4RA	JPW	rev	172	143	84	30	9.83	100	320	>1	
31-G4	LAP4RB	JPW	rev	139	115	70	64	9.89	100	270	>1	
32-H4	LAP4RC	JPW	rev	160	119	78	65	9.85	98	280	>1	

Analyzed by: **ASP**

loaded by: **ASP**   Folder: _Full length + scientists_

Factura/Blast Analysis:

Additional Comments: _Retracted JN_

Human Genome Sciences, Inc.

Plate I.D.(s) _____ _____

'ate Initiated: _____

Date Completed: _____

Results Folder: _8·19.94 17HG?_

% Good: _____   **% Good:** _____

Templates	Sequence Reaction	Gel Run
Method:	Method: manuals	Machine ID: 17
Prep Person:	Prep Person: karen	Gel Loader:renee
Prep Date:	Prep Date: 8/18/94	Run Date:8/18/94

#	Sample Name	Scientist name/init	Primer DP/DT	C	A	G	T	Base Spacing	vector	Edited length	% Ns	Trash Code
1-A1	HSUSH20S13RP01	ANN KIM	6800	28	53	85	52	9.00		310		
2-B1	HSUSH20S14RP01	ANN KIM	6800	31	56	90	55	9.00		350		
3-C1	HSUSH20S15RP01	ANN KIM	6800	87	159	23	117	9.00		380		
4-D1	HSUSH20S16RP01	ANN KIM	6800	98	86	144	77	9.00		340		
5-E1	HSUSH20S17RP01	ANN KIM	6800	27	42	67	52	9.00		290		
6-F1	HSUSH20S18RP01	ANN KIM	6800	20	31	40	48	9.00		290		
7-G1	HSUSH20S19RP01	ANN KIM	6800	19	28	42	35	9.00		290		
8-H1	HSUSH20S20RP01	ANN KIM	6800	14	19	26	35	-1200		290		
9-A2	HSUSH20S21RP01	ANN KIM	6800	53	94	137	107	9.00		355		
10-B2	HSUSH20S22RP01	ANN KIM	6800	29	46	53	75	9.00		250		
11-C2	HSUSH20S23RP01	ANN KIM	6800	46	93	18	100	9.00		320		
12-D2	HSUSH20S24RP01	ANN KIM	6800	27	41	43	36	9.00		320		
13-E2	HSUSH20S25RP01	ANN KIM	6800	33	35	33	18	-1200				R
14-F2	HSUSH20S13FP04	ANN KIM	6987	64	111	155	122	9.00		460		
15-G2	HSUSH20S14FP04	ANN KIM	6987	32	52	71	51	9.00		350		
16-H2	HSUSH20S15FP04	ANN KIM	6987	91	116	194	162	9.00		310		
17-A3	HSUSH20S16FP04	ANN KIM	6987	54	139	178	164	9.00		350		
18-B3	HSUSH20S17FP04	ANN KIM	6987	61	98	61	55	9.00		380		
19-C3	HSUSH20S18FP04	ANN KIM	6987	73	35	43	73	-1200		300		
20-D3	HSUSH20S19FP04	ANN KIM	6987	34	18	47	75	9.00		340		
21-E3	HSUSH20S20FP04	ANN KIM	6987	13	12	18	44	-1200				R
22-F3	HSUSH20S21FP04	ANN KIM	6987	65	115	160	112	9.00		390		
23-G3	HSUSH20S22FP04	ANN KIM	6987	27	39	46	57	9.00		340		
24-H3	HSUSH20S23FP04	ANN KIM	6987	56	101	163	16	9.00		330		
25-A4	HSUSH20S24FP04	ANN KIM	6987	36	73	73	88	9.00		350		
26-B4	HSUSH20S25FP04	ANN KIM	6987	77	41	43	76	9.00		290		
27-C4	HSUSH20RP01B	ANN KIM	6800	68	126	189	135	9.00		410		
28-D4	HSUSH20FP04	ANN KIM	6987	48	78	123	99	9.00		480		
29-E4	HTPAN08S04RP01d	ANN KIM	685	85	655	27	27	9.00		330		
30-F4	HTPAN08S04RP03d	ANN KIM	5424	74	303	308	402	9.00		380		
31-G4	HTPAN08S04RP05d	ANN KIM	5426	66	391	115	136			290		
32-H4	BLUESCRIPTDT	CONTROL		52	96	137	138	9.00		450		

.nalyzed by: _PYS_

Uploaded by: _eve_   Folder: _FL/SS._

Factura/Blast Analysis: _____

Additional Comments:

Bluescript : 8/3/94

OT RXN MIX : 848-003

TIPS : 40628433

Silent Monitor : 099311

Tubes : P16J4

Human Genome Sciences, Inc.

Plate I.D.(s) _____ _____

Date Initiated: _____

Date Completed: _____

% Good: _____ % Good: _____

Templates	Sequence Reaction	Gel Run
Method:	Method: manual	Machine ID: 18
Prep Person:	Prep Person: karen	Gel Loader: renee
Prep Date:	Prep Date: 8/18/94	Run Date: 8/18/94

#	Sample Name	Scientist name/init	Primer DP/DT	C	A	G	T	Base Spacing	vector	Edited length	% Ns	Trash Code
1-A5	HTPAN08S04RP06d	ANN KIM	5676	90	305	296	29	0.00		370		
2-B5	HTPAN08S04RP07d	ANN KIM	5688	51	213	30	447	9.00		250		
3-C5	HTPAN08S04RP10d	ANN KIM	6442	53	420	29	250	9.00		350		
4-D5	HTPAN08S04RP12d	ANN KIM	6638	72	508	213	223	9.00		246		
5-E5	HTPAN08S04RP14d	ANN KIM	6640	130	288	377	377	9.00		348		
6-F5	HTPAN08S04FP15d	ANN KIM	6813	52	148	173	63	70.00				L
7-G5	HTPAN08S04FP16d	ANN KIM	7409	105	296	341	204	9.00		270		
8-H5	HTPAN08S04FP17d	ANN KIM	7408	153	323	30	590	9.00		200		
9-A6	HTPAN08S04FP118d	ANN KIM	7407	86	273	296	40	9.00		380		
10-B6	HTPAN08S04RP19d	ANN KIM	7406	83	20	78	65	9.00		375		
11-C6	HTPAN08S04RP20d	ANN KIM	7405	30	438	25	172	9.00		360		
12-D6	HTCCI56ARP01	ANN KIM	685	45	50	118	163	9.00		290		
13-E6	HTCCI56ARP03	ANN KIM	5424	59	213	209	359	-12.00				L
14-F6	HTCCI56ARP05	ANN KIM	5426	51	373	144	24	9.00		295		
15-G6	HTCCI56ARP06	ANN KIM	5676	211	351	108	122	0.00		168		
16-H6	HTCCI56ARP07	ANN KIM	5688	55	172	190	371	9.00		120		
17-A7	HTCCI56ARP10	ANN KIM	6442	59	274	126	176	9.00		300		
18-B7	HTCCI56ARP12	ANN KIM	6638	90	60	239	296	9.00		236		
19-C7	HTCCI56ARP14	ANN KIM	6640	100	109	296	335	0.00		260		
20-D7	HTCCI56AFP15	ANN KIM	6813	43	110	136	213	-12.00				L
21-E7	HTCCI56AFP16	ANN KIM	7409	70	167	123	158	9.00		296		
22-F7	HTCCI56AFP17	ANN KIM	7408	46	59	91	129	9.00		300		
23-G7	HTCCI56AFP18	ANN KIM	7407	411	113	102	178	9.00		300		
24-H7	HTCCI56ARP19	ANN KIM	7406	77	481	161	266	9.00		270		
25-A8	HTCCI56ARP20	ANN KIM	7405	60	33	270	233	-10.00		340		
26-B8	HOSDK13ARP03	ANN KIM	5424	88	304	286	355	9.00		337		
27-C8	HOSDK13ARP07	ANN KIM	5688	64	201	249	159	9.00		150		
28-D8	HOSDK13AFP15	ANN KIM	6813	33	85	95	167	9.00		280		
29-E8	HOSDK13ARP19	ANN KIM	7406	111	500	190	333	0.00		310		
30-F8	HOSDK13ARP20	ANN KIM	7405	119	65	39	30	9.00		270		
31-G8	bluescriptDT	CONTROL		51	103	117	137	9.00		380		
32-H8												

analyzed by: PYS

Uploaded by: LYS Folder: FL/SS

Factura/Blast Analysis: _____

Additional Comments:
Bluescript: 8/3/94
RXN Mix: 848-003
Tips 40628433

Silent Monitor: 099-311
Tubes: P1054

102

Human Genome Sciences, Inc.

Plate I.D.(s) _____ _____

Date Initiated: _____

Results Folder: 8-19-94 18 HGS

Date Completed: _____

% Good: _____   % Good: _____

Templates	Sequence Reaction	Gel Run
Method:	Method: manual	Machine ID: 18
Prep Person:	Prep Person: karen	Gel Loader: renee
Prep Date:	Prep Date: 8/18/94	Run Date: 8/18/94

#	Sample Name	Scientist name/init	Primer DP/DT	C	A	G	T	Base Spacing	vector	Edited length	% Ns	Trash Code
1-A5	HTPAN08S04RP06d	ANN KIM	5676	9C	305	296	279	9.00		370		
2-B5	HTPAN08S04RP07d	ANN KIM	5688	51	273	307	447	9.00		280		
3-C5	HTPAN08S04RP10d	ANN KIM	6442	5.3	420	29	250	9.00		360		
4-D5	HTPAN08S04RP12d	ANN KIM	6638	27	508	213	273	9.00		240		
5-E5	HTPAN08S04RP14d	ANN KIM	6640	130	88	377	367	9.00		378		
6-F5	HTPAN08S04FP15d	ANN KIM	6813	62	148	173	63	72.00				R
7-G5	HTPAN08S04FP16d	ANN KIM	7409	105	376	244	204	9.00		270		
8-H5	HTPAN08S04FP17d	ANN KIM	7408	153	373	361	597	9.00		200		
9-A6	HTPAN08S04FP118d	ANN KIM	7407	86	213	306	472	9.00		320		
10-B6	HTPAN08S04RP19d	ANN KIM	7406	83	249	148	205	9.00		375		
11-C6	HTPAN08S04RP20d	ANN KIM	7405	54	433	229	172	9.00		380		
2-D6	HTCCI56ARP01	ANN KIM	685	45	50	113	163	9.00		240		
13-E6	HTCCI56ARP03	ANN KIM	5424	59	213	209	359	-12.00				R
14-F6	HTCCI56ARP05	ANN KIM	5426	51	373	144	274	9.00		348		
15-G6	HTCCI56ARP06	ANN KIM	5676	211	351	108	122	9.00		168		
16-H6	HTCCI56ARP07	ANN KIM	5688	55	172	190	271	9.00		120		
17-A7	HTCCI56ARP10	ANN KIM	6442	52	274	136	136	9.00		300		
18-B7	HTCCI56ARP12	ANN KIM	6638	90	160	239	296	9.00		236		
19-C7	HTCCI56ARP14	ANN KIM	6640	100	109	244	338	9.00		260		
20-D7	HTCCI56AFP15	ANN KIM	6813	43	110	134	213	72.00				R
21-E7	HTCCI56AFP16	ANN KIM	7409	70	167	123	155	9.00		298		
22-F7	HTCCI56AFP17	ANN KIM	7408	48	59	91	179	9.00		300		
23-G7	HTCCI56AFP18	ANN KIM	7407	41	113	108	178	9.00		300		
24-H7	HTCCI56ARP19	ANN KIM	7406	77	481	161	266	9.00		270		
25-A8	HTCCI56ARP20	ANN KIM	7405	96	353	240	228	-12.00		390		
26-B8	HOSDK13ARP03	ANN KIM	5424	88	32	286	55	9.00		397		
27-C8	HOSDK13ARP07	ANN KIM	5688	64	361	249	459	9.00		150		
28-D8	HOSDK13AFP15	ANN KIM	6813	37	75	95	167	9.00		280		
29-E8	HOSDK13ARP19	ANN KIM	7406	111	500	190	373	9.00		310		
30-F8	HOSDK13ARP20	ANN KIM	7405	119	665	311	352	9.00		270		
31-G8	bluescriptDT	CONTROL		51	103	117	127	9.00		380		
32-H8												

Analyzed by: RYS

Uploaded by: RYS   Folder: FL/SS

Factura/Blast Analysis: _____

Additional Comments:

Bluescript: 8/3/94

RXN Mix: 848-003

Tips 40628433

Silent Monitor: 099-311

Tubes: P1654

103

Human Genome Sciences, Inc.

Plate I.D.(s) _____ _____

Templates	Sequence Reaction	Gel Run
Method:	Method: manual	Machine ID: 18
Prep Person:	Prep Person: karen	Gel Loader: renee
Prep Date:	Prep Date: 8/18/94	Run Date: 8/18/94

#	Sample Name	Scientist name/init.	Primer DP/DT	C	A	G	T	Base Spacing	vector	Edited length	% Ns	Trash Code
1-A5	HTPAN08S04RP06d	ANN KIM	5676	9C	55	296	39	9.00		375		
2-B5	HTPAN08S04RP07d	ANN KIM	5688	81	273	30	447	9.00		280		
3-C5	HTPAN08S04RP10d	ANN KIM	6442	53	420	29	250	9.00		350		
4-D5	HTPAN08S04RP12d	ANN KIM	6638	82	508	23	283	9.0G		290		
5-E5	HTPAN08S04RP14d	ANN KIM	6640	130	08	377	347	9.00		376		
6-F5	HTPAN08S04FP15d	ANN KIM	6813	52	148	183	63	72.00				R
7-G5	HTPAN08S04FP16d	ANN KIM	7409	105	376	244	304	9.00		270		
8-H5	HTPAN08S04FP17d	ANN KIM	7408	153	303	361	597	9.00		200		
9-A6	HTPAN08S04FP118d	ANN KIM	7407	86	233	246	42	9.00		300		
10-B6	HTPAN08S04RP19d	ANN KIM	7406	83	249	78	235	9.00		375		
11-C6	HTPAN08S04RP20d	ANN KIM	7405	53	453	29	172	9.00		380		
2-D6	HTCCI56ARP01	ANN KIM	685	45	570	118	163	9.00		290		
13-E6	HTCCI56ARP03	ANN KIM	5424	59	213	209	359	-12.00				R
14-F6	HTCCI56ARP05	ANN KIM	5426	51	373	144	34	9.00		245		
15-G6	HTCCI56ARP06	ANN KIM	5676	211	251	108	122	9.00		168		
16-H6	HTCCI56ARP07	ANN KIM	5688	55	176	190	271	9.00		120		
17-A7	HTCCI56ARP10	ANN KIM	6442	59	271	156	176	9.00		300		
18-B7	HTCCI56ARP12	ANN KIM	6638	90	610	237	296	9.00		236		
19-C7	HTCCI56ARP14	ANN KIM	6640	100	109	296	338	9.00		260		
20-D7	HTCCI56AFP15	ANN KIM	6813	43	110	136	213	-72.00				R
21-E7	HTCCI56AFP16	ANN KIM	7409	70	167	123	155	9.00		290		
22-F7	HTCCI56AFP17	ANN KIM	7408	42	59	91	129	9.00		300		
23-G7	HTCCI56AFP18	ANN KIM	7407	41	113	122	178	9.00		300		
24-H7	HTCCI56ARP19	ANN KIM	7406	77	481	161	266	9.00		270		
25-A8	HTCCI56ARP20	ANN KIM	7405	60	333	210	222	-12.00		310		
26-B8	HOSDK13ARP03	ANN KIM	5424	88	331	286	55	9.00		337		
27-C8	HOSDK13ARP07	ANN KIM	5688	64	301	249	459	9.00		150		
28-D8	HOSDK13AFP15	ANN KIM	6813	32	55	95	167	9.00		280		
29-E8	HOSDK13ARP19	ANN KIM	7406	111	560	190	273	0.00		310		
30-F8	HOSDK13ARP20	ANN KIM	7405	114	615	311	251	9.00		270		
31-G8	bluescriptDT	CONTROL		51	103	114	137	9.00		380		
32-H8												

Analyzed by: PYS

Uploaded by: LYS   Folder: FL/SS

Additional Comments:

Bluescript: 8/3/94

RXN Mix: 848-003

Tips 40628433

Factura/Blast Analysis: _____

Silent Monitor: 099-311

Tubes: P1654

Human Genome Sciences, Inc.

Plate I.D.(s) _____ . _____

Date Initiated: _____

Date Completed: **8-20-94**

Results Folder: **08/20/94   39   HGS**

% Good: _____   % Good: _____

Templates	Sequence Reaction	Gel Run
Method: MISC	Method: BIOMEK/MANUAL	Machine ID: **39**
Prep Person: MISC	Prep Person: **SMR/ASP**	Gel Loader: **ASP**
Prep Date: MISC	Prep Date: 08/19/94	Run Date: **8/19/94**

#	Sample Name	Scientist name/init	Primer DP/DT for	C	A	G	T	Base Spacing	vector	Edited length	% Ns	Trash Code
1-A1	bluescript	Control	for	147	227	154	158	9.37	70	430	3N/16	
2-B1	HOSAA69F	HLJ	FOR	271	135	151	116	9.23	—			R
3-C1	HOSAA70F	HLJ	FOR	174	137	71	53	9.31	—			T
4-D1	HOSAA71F	HLJ	FOR	111	134	63	41	9.30	76	146	5%	
5-E1	HMEDM76F	HLJ	FOR	37	41	24	21	9.28				R
6-F1	HTTCA40AF	ANN KIM	for	94	124	41	49	9.34	70	425	6N/14	
7-G1	HTTCA40BF	ANN KIM	for	269	839	70	144	9.33	70	409	5N/12	
8-H1	bluescript	Control	rev	166	240	114	123	9.42	93	305	13/44	
9-A2	HCEBM41Ra	Kunsch	REV	258	169	79	70	9.40	93	357	4N/14	
10-B2	HCEBM41Rb	Kunsch	REV	339	249	120	103	9.35	93	337	3N/41	
11-C2	HOSAA69R	HLJ	REV	173	135	87	80	9.52	93			
2-D2	HOSAA70R	HLJ	REV	142	126	77	69	9.46	95			R
13-E2	HOSAA71R	HLJ	REV	151	141	51	65	9.41	95	255	6N/21	L
14-F2	rpb3ra	paul	REV	371	292	156	140	9.45	92			
15-G2	he2cb95ra	paul	REV	152	621	277	332	9.35	92	268	3N/41	M
16-H2	hhpft46ra	paul	REV	258	198	98	105	9.39	93	347	4N/11	
17-A3	httck42ra	paul	REV									
18-B3	hhfbt61ra	paul	REV	520	298	204	166	9.36	93	340	2N/14	N
19-C3	H32EQ28R	soppet/g	REV	443	353	161	159	9.35	93	387	4N/41	
20-D3	HHF8D38R	soppet/g	REV	402	267	179	165	9.34	95	353	8N/41	
21-E3	HETBV89R	soppet/g	REV	648	443	243	260	9.41	93	357	4N/41	
22-F3	HTTCA40AR	ANN KIM	REV	77	77	36	37	9.31	100	325	3N/41	
23-G3	HTTCA40BR	ANN KIM	REV	413	378	182	113	9.34	92	338	3N/41	
24-H3	bluescript	Control	rev	356	249	126	144	9.41	92	325	6N/41	
25-A4												
26-B4												
27-C4												
28-D4												
29-E4												
30-F4												
31-G4												
32-H4												

Analyzed by: _Julie_

Uploaded by: _Julie_   Folder: _Fulllength/Scientists_

Factura/Blast Analysis: _____

Additional Comments:

Applied Biosystems

Synthesis Order - 7689 HTPAN08 5'BAM HI

Run date: 8/30/94
Run ID: 7689
Customer: ANN KIM

1.
2.
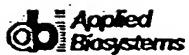Synthesizer: Synthesizer-2
Model: 394-08
ROM version: 2.00

Sequence name: 7689 HTPAN08 5'BAM HI
Sequence: CCGCG CGG ATC CAC CAT GGC TGGAT GAT GGA GGT C

Cycle: 40 nM CE

End procedure: End CESS
DMT: Off

Comments:
Sent to "Synthesizer-2" col 1 seq 31 at 8/31/94 9:58 AM.

Handwritten annotations:

GCC A/GCC ATG G
         -3 T   +4

GGA TCC GCG GCC
A

w/ ATG Site from
Clone

GCC ATC
G
G/
GCC ATC

G... GGA TCC ATC ATG
      Bam   KOZAZ   m

Applied Biosystems

Synthesis Order - 7690 HTPAN08 3'ASP 718

Run date: 8/30/94
Run ID: 7690
Customer: ANN KIM

1.
2.
Synthesizer: Synthesizer-2
Model: 394-08
ROM version: 2.00

Sequence name: 7690 HTPAN08 3'ASP 718
Sequence: GCG CGG TAC CAG TTA GCC AAC TAA AAA GGC CCC G

Cycle: 40 nM CE

End procedure: End CESS
DMT: Off

Comments:
Sent to "Synthesizer-2" col 2 seq 32 at 8/31/94 9:59 AM.

including Stop + Additional Seq.

T A 4

Human Genome ~iences, Inc.

Pl~ .D.(s) _____ _____

Date Initiated: _____
Date Completed: _09·13·94_

Results Folder: _09·13·94 23 HGS_
% Good: _____ % Good: _____

Templates	Sequence Reaction	Gel Run
Method:	Method: MANUAL	Machine ID: 2 3
Prep Person:	Prep Person: GRP	Gel Loader: JJm
Prep Date:	Prep Date: 09/12/94	Run Date: 09·12·94

#	Sample Name	Scientist name/init. control	Primer DP/DT	Signal Strength G	A	G	C	Base Spacing	vector	Edited length	% Ns	Trash Code
1-A1	BLUESCRIPT			242	156	56	76	10.01	20	440		
2-b1	htaac10s23fp23	fischer										N
3-C1	htaac10s03fp23	fischer										N
4-D1	HTAAC10S02RP29	FISCHER										N
5-E1	HTAAC10S48RP25	FISCHER										N
6-F1	HTAAC10S57RP26	FISCHER										N
7-G1	HTAAC10S01RP28	FISCHER										N
8-H1	HTAAC10S03RP24	FISCHER		100	638	158	46	9.86	60	330		
9-A2	hjuaa13206	paul		154	153	57	55	9.89	10	410		
10-B2	hjuaa13233	paul		142	103	45	39	9.90	10	330		
11-C2	hjuaa13490	paul		163	96	55	35	9.92	30	320		
12-D2	hjuaa13491	paul		223	147	60	53	9.89	30	410		
13-E2	HTPAN08B05RP05A	ANN KIM		222	254	100	46	9.90	10	340		
14-F2	HTPAN08B05RP06A	ANN KIM		154	173	72	37	9.95	30	300		
15-G2	HTPAN08B03RP05A	ANN KIM		192	232	90	40	9.90	20	400		
16-H2	HTPAN08B03RP06A	ANN KIM		207	212	90	45	9.95	30	340		
17-A3	HTPAN08B03FP14A	ANN KIM		158	110	76	37	9.91	30	400		
18-B3	HTPAN08B03FP14A	ANN KIM		158	129	99	42	9.86	30	420		
19-C3	HTPAN08B04RP06A	ANN KIM		175	201	105	44	9.73	50	340		
20-D3	HTPAN08B04RP10A	ANN KIM		137	152	55	32	9.80	50	330		
21-E3	HTPAN08B01RP06A	ANN KIM		175	167	72	36	9.84	20	370		
22-F3	HTPAN08B01FP14A	ANN KIM		218	145	91	44	9.87	20	400		
23-G3	HTPAN08B02RP06A	FISCHER A										N
24-H3	HTPAN08B02RP10A	FISCHER		131	143	59	30	9.82	20	360		
25-A4	HTAAC10S01FP23A	FISCHER		178	170	92	66	9.70	40	380		
26-B4	HTAAC10S57FP23A	FISCHER		165	110	70	60	9.88	30	410		
27-C4	HSSNB01S01RP07A	KUNSCH		254	174	67	77	9.95	60	300		
28-D4	HSSNB01S01RP08A	KUNSCH		310	255	95	133	9.89	70	320		
29-E4	HATBG78RP23A	ZHEN LI		169	121	65	59	9.75	20	400		
30-F4	HPLBQ88RP01fA	HLA		275	204	79	82	9.94	30	340		
31-G4	HPLBQ88FP01fA	HLA		235	103	75	77	-12.00				R
32-H4	HPLBQ88FP01iA	HLA		116	52	41	37	10.16	50	340		

Analyzed by: _JJm_
Uploaded by: _JJm_   Folder: _FL/SC1_

Factura/Blast Analysis: _____

* k.. ~ v~l.i<lc~2)

Applied Biosystems

Synthesis Order - 2499 HTPAN08S04 3' XBA

Run date: 9/26/94
Run ID: 2499
Customer: ANN KIM

1.   CX
2.
Synthesizer: Synthesizer-2
Model: 394-08
RCM version: 2.00

Sequence name: HTPAN08S04 3'XBA - PD10
Sequence: GCG AGA TCT CAG TTA GCC AAC TAA AAA GGC CCC GAA

Cycle: 40 nM CE

End procedure: End CESS
DMT: Off

Comments:

Sent to "Synthesizer-2" col 1 seq 31 at 9/27/94 7:01 AM.

109

Synthesis Order - 2500 HTPAN08S04 5'BAM HI

Run date: 9/26/94
Run ID: 2500
Customer: ANN KIM

1.   CX
2.
Synthesizer: Synthesizer-2
Model: 394-08
ROM version: 2.00

Sequence name: HTPAN08S04 5' BAM HI -PD10
Sequence: GGG GGA TTC AAG CAG ATG CAG GAC AAG TAC TCC AAA

Cycle: 40 nM CE

End procedure: End CESS
DMT: Off

Comments:
Sent to "Synthesizer-2" col 2 seq 32 at 9/27/94 7:02 AM.

110

Applied Biosystems

Synthesis Order - 2656 htpan08s04 3'xba

Run date: 10/26/94
Run ID: 2656 AMK
Customer: a kim

1.   KH
2.
Synthesizer: Synthesizer-2
Model: 394-08
ROM version: 2.00

Sequence name: 2656 htpan08s04 3'xba
Sequence: CGC GCG AGA TCT CAG TTA GCC AAC TTA AAA GGC C

Cycle: 40 nM CE

End procedure: End CESS
DMT: Off

Comments:

ᴥᴥ Applied
ᴥᴥ Biosystems
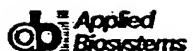
Synthesis Order - 2751 htpan08s04 5'bam new

Run date: 11/7/94
Run ID: 2751 AMK
Customer: a kim

1.   CRG
2.
Synthesizer: None
Model:
ROM version:

Sequence name: htpan08s04 5'bam new
Sequence: GCG GCG GGA TCC ATG GGC TAT GAT GGA GGT CCA

Cycle:

End procedure:
DMT: Off

Comments:

 SYNTHESIZED ON 3948

Translate DNA Sequence htpan08 185bporf(1,714)
With Standard Genetic Code

Molecular Weight 27689.30 Daltons
237 Amino Acids
31 Strongly Basic(+) Amino Acids (K,R)
30 Strongly Acidic(-) Amino Acids (D,E)
65 Hydrophobic Amino Acids (A,I,L,F,W,V)
79 Polar Amino Acids (N,C,Q,S,T,Y)

7.857 Isolectric Point
1.842 Charge at PH 7.0

Total number of bases translated is 714
% A = 34.59
% G = 21.43
% T = 25.07
% C = 18.91
% Ambiguous 0.00

% A+T = 59.66
% C+T = 43.98

Davis,Botstein,Roth Melting Temp C. 80.74
Wallace Temp C   2274.00

Codon usage:

codon	aa	n		codon	aa	n		codon	aa	n		codon	aa	n
acg	( )	0	#	gau	Asp(D)	2	#	---	Ilu(I)	15	#	uca	Ser(S)	3
ccg	( )	0	#	---	Asp(D)	11	#	cua	Leu(L)	1	#	ucc	Ser(S)	5
cgg	( )	0	#	ugc	Cys(C)	1	#	cuc	Leu(L)	3	#	ucu	Ser(S)	7
gcg	( )	0	#	ugu	Cys(C)	2	#	cug	Leu(L)	3	#	---	Ser(S)	26
uag	( )	0	#	---	Cys(C)	3	#	cuu	Leu(L)	1	#	uaa	Ter(.)	1
ucg	( )	0	#	caa	Gln(Q)	9	#	uua	Leu(L)	2	#	---	Ter(.)	1
uga	( )	0	#	cag	Gln(Q)	4	#	uug	Leu(L)	7	#	aca	Thr(T)	6
---	( )	0	#	---	Gln(Q)	13	#	---	Leu(L)	17	#	acc	Thr(T)	3
gca	Ala(A)	2	#	gaa	Glu(E)	14	#	aaa	Lys(K)	9	#	acu	Thr(T)	1
gcc	Ala(A)	2	#	gag	Glu(E)	5	#	aag	Lys(K)	8	#	---	Thr(T)	10
gcu	Ala(A)	4	#	---	Glu(E)	19	#	---	Lys(K)	17	#	ugg	Trp(W)	5
---	Ala(A)	8	#	gga	Gly(G)	3	#	aug	Met(M)	6	#	---	Trp(W)	5
aga	Arg(R)	9	#	ggc	Gly(G)	3	#	---	Met(M)	6	#	uac	Tyr(Y)	6
agg	Arg(R)	2	#	ggg	Gly(G)	5	#	uuc	Phe(F)	3	#	uau	Tyr(Y)	7
cga	Arg(R)	1	#	ggu	Gly(G)	2	#	uuu	Phe(F)	7	#	---	Tyr(Y)	13
cgc	Arg(R)	1	#	---	Gly(G)	13	#	---	Phe(F)	10	#	gua	Val(V)	2
cgu	Arg(R)	1	#	cac	His(H)	3	#	cca	Pro(P)	1	#	guc	Val(V)	3

113

---	Arg(R)	14	#	cau	His(H)	3	#	ccc	Pro(P)	3	#	gug	Val(V)	1
?ac	Asn(N)	7	#	---	His(H)	6	#	ccu	Pro(P)	3	#	guu	Val(V)	4
aau	Asn(N)	7	#	aua	Ilu(I)	6	#	---	Pro(P)	7	#	---	Val(V)	10
---	Asn(N)	14	#	auc	Ilu(I)	3	#	agc	Ser(S)	3	#	nnn	???(X)	0
gac	Asp(D)	9	#	auu	Ilu(I)	6	#	agu	Ser(S)	8	#	TOTAL		238

```
          10          20          30          40
   |....|....|....|....|....|....|....|....|
MQDKYSKSGI ACFLKEDDSY WDPNDEESMN SPCWQVKWQL 40
RQLVRKMILR TSEETISTVQ EKQQNISPLV RERGPQRVAA 80
HITGTRGRSN TLSSPNSKNE KALGRKINSW ESSRSGHSFL 120
SNLHLRNGEL VIHEKGFYYI YSQTYFRFQE EIKENTKNDK 160
QMVQYIYKYT SYPDPILLMK SARNSCWSKD AEYGLYSIYQ 200
          210         220         230         240
   |....|....|....|....|....|....|....|....|
GGIFELKEND RIFVSVTNEH LIDMDHEASF FGAFLVG. 238
```

114

Translate DNA Sequence htpan08orf(1,846)
With Standard Genetic Code

    Molecular Weight 32511.50 Daltons
    281 Amino Acids
    32 Strongly Basic(+) Amino Acids (K,R)
    32 Strongly Acidic(-) Amino Acids (D,E)
    84 Hydrophobic Amino Acids (A,I,L,F,W,V)
    94 Polar Amino Acids (N,C,Q,S,T,Y)

    7.324 Isolectric Point
    0.784 Charge at PH 7.0

    Total number of bases translated is 846
    % A = 32.27
    % G = 22.81
    % T = 25.06
    % C = 19.86
    % Ambiguous 0.00

    % A+T = 57.33
    % C+T = 44.92

    Davis,Botstein,Roth Melting Temp C. 81.80
    Wallace Temp C   2750.00
Codon usage:

acg	( )	0	#	gau	Asp(D)	2	# ---	Ilu(I)	17	# uca	Ser(S)	3
ccg	( )	0	# ---	Asp(D)	11	# cua	Leu(L)	1	# ucc	Ser(S)	5
cgg	( )	0	# ugc	Cys(C)	2	# cuc	Leu(L)	5	# ucu	Ser(S)	8
gcg	( )	0	# ugu	Cys(C)	3	# cug	Leu(L)	7	# ---	Ser(S)	28
uag	( )	0	# ---	Cys(C)	5	# cuu	Leu(L)	1	# uaa	Ter(.)	1
ucg	( )	0	# caa	Gln(Q)	9	# uua	Leu(L)	2	# ---	Ter(.)	1
uga	( )	0	# cag	Gln(Q)	8	# uug	Leu(L)	7	# aca	Thr(T)	7
---	( )	0	# ---	Gln(Q)	17	# ---	Leu(L)	23	# acc	Thr(T)	5
gca	Ala(A)	2	# gaa	Glu(E)	14	# aaa	Lys(K)	9	# acu	Thr(T)	2
gcc	Ala(A)	2	# gag	Glu(E)	7	# aag	Lys(K)	9	# ---	Thr(T)	14
gcu	Ala(A)	6	# ---	Glu(E)	21	# ---	Lys(K)	18	# ugg	Trp(W)	5
---	Ala(A)	10	# gga	Gly(G)	5	# aug	Met(M)	9	# ---	Trp(W)	5
aga	Arg(R)	9	# ggc	Gly(G)	3	# ---	Met(M)	9	# uac	Tyr(Y)	8
agg	Arg(R)	2	# ggg	Gly(G)	6	# uuc	Phe(F)	4	# uau	Tyr(Y)	7
cga	Arg(R)	1	# ggu	Gly(G)	2	# uuu	Phe(F)	8	# ---	Tyr(Y)	15
cgc	Arg(R)	1	# ---	Gly(G)	16	# ---	Phe(F)	12	# gua	Val(V)	3
cgu	Arg(R)	1	# cac	His(H)	3	# cca	Pro(P)	1	# guc	Val(V)	4

---	Arg(R)	14	#	cau	His(H)	3	#	ccc	Pro(P)	4	#	gug	Val(V)	6
aac	Asn(N)	8	#	---	His(H)	6	#	ccu	Pro(P)	3	#	guu	Val(V)	4
aau	Asn(N)	7	#	aua	Ilu(I)	6	#	---	Pro(P)	8	#	---	Val(V)	17
---	Asn(N)	15	#	auc	Ilu(I)	5	#	agc	Ser(S)	4	#	nnn	???(X)	0
gac	Asp(D)	9	#	auu	Ilu(I)	6	#	agu	Ser(S)	8	#	TOTAL		282

```
          10         20         30         40
....|....| ....|....| ....|....| ....|....|
MAMMEVQGGP SLGQTCVLIV IFTVLLQSLC VAVTYVYFTN  40
ELKQMQDKYS KSGIACFLKE DDSYWDPNDE ESMNSPCWQV  80
KWQLRQLVRK MILRTSEETI STVQEKQQNI SPLVRERGPQ 120
RVAAHITGTR GRSNTLSSPN SKNEKALGRK INSWESSRSG 160
HSFLSNLHLR NGELVIHEKG FYYIYSQTYF RFQEEIKENT 200

         210        220        230        240
....|....| ....|....| ....|....| ....|....|
KNDKQMVQYI YKYTSYPDPI LLMKSARNSC WSKDAEYGLY 240
SIYQGGIFEL KENDRIFVSV TNEHLIDMDH EASFFGAFLV 280
G. 282
```

```
                          10        20        30        40        50        60
                     ....|....|....|....|....|....|....|....|....|....|....|....|
HTPAN08P185FP16(1>164) <-  CTTAAGGATGATTGRCCAGAA-TCTCTGATTCTGTAGCACATGACTNACTTGCTAGACAT
HTPAN08P185RP50(1>226) ->                     ACTCGCAAATAAATAAGTATTTTACTGTGTTCGTA-ACAG
                                              _____
                           CTTAAGGATGATTGACCAGAA-TCGCAAATAAAGAAGCACATGACTGACTTCCTA-ACAG


                          70        80        90       100       110       120
                     ....|....|....|....|....|....|....|....|....|....|....|....|
HTPAN08P185FP16(1>164) <-  GGWTGTTG-AAGCCAGACCTATCGAGACCCYGGWAGATGCATAMCCTCY-A-GAYWTCGG
HTPAN08P185RP50(1>226) ->  TGTTGTAATAAAAAA-ACCTATRAATATTCCGGATTATTCATACCGTCCCACCA--TCGG
HTPAN08P185FP14(1>338) <-                           GGWAGATGCATAMCCTCY-A-GAYTTCGG
HTPAN08P185FP08(1>388) <-                               ATGCATAACCTCT-AAGACWTCGG
                                                          _____
                           GGTTGTAA-AAAAAA-ACCTATCAAGACCCCGGAAGATGCATAACCTCC-A-GACTTCGG


                         130       140       150       160       170       180
                    ....|....|....|....|....|....|....|....|....|....|....|....|
HTPAN08P185FP16(1>164) <-  GGTTGGAT-CCATCATGCAGGACAAGTACTCCAAMAGTGNCATTGCTTG
HTPAN08P185RP50(1>226) ->  GGGCGGAT-CCATCATGSAGGACAAGTNCTCCAAAAGTGGTATTGCTTGTTTCTTAATAG
HTPAN08P185FP14(1>338) <-  GSGTGGAT-CCATCATGCAGGACAAGTACKCCMCCAGTGGCATTGCTTGTTTYTTAAAAG
HTPAN08P185FP08(1>388) <-  GGKTGGATCCCATCATGCAGGACAAGTACTCCAAAAGTGNCATTGCTTGTTTCGTAAAAG
htpan08 185bporf(1>714)->           ATGCAGGACAAGTACTCCAAAAGTGGCATTGCTTGTTTCTTAAAAG
                                   _____
                           GGGTGGAT-CCATCATGCAGGACAAGTACTCCAAAAGTGGCATTGCTTGTTTCTTAAAAG


                         190       200       210       220       230       240
                    ....|....|....|....|....|....|....|....|....|....|....|....|
HTPAN08P185RP50(1>226) ->  AGGATGACAGYTATTGGGACCCC-AATGACGAAGAGAGTATGAACAGCCCCTGCTGGCAA
HTPAN08P185FP14(1>338) <-  AAGATGACAGTTATTGGGACCCC-AATGACGAAGAGAGTATGGACAGCCCCTGCTGGCAA
HTPAN08P185FP08(1>388) <-  AAGATGACAGTTATTGGGACCCCCAATGACGAAGAGAGTATGAACARCCCCTKCTGRCAA
htpan08 185bporf(1>714)->  AAGATGACAGTTATTGGGACCCC-AATGACGAAGAGAGTATGAACAGCCCCTGCTGGCAA
                           _____
                           AAGATGACAGTTATTGGGACCCC-AATGACGAAGAGAGTATGAACAGCCCCTGCTGGCAA


                         250       260       270       280       290       300
                    ....|....|....|....|....|....|....|....|....|....|....|....|
HTPAN08P185RP50(1>226) ->  TGTCAAGTGGCA
HTPAN08P185FP14(1>338) <-  -GTCAAGTGGCAACTCCGTCAGCTCGTTAGAAAGATGATTTTGAGAACCTCTGAGGAAAC
HTPAN08P185FP08(1>388) <-  -GTCAAGTGGCAACTCCGTCAGCTCGTTAGAAAGATGATTTTGAGAACCTCTGAGGAAAC
htpan08 185bporf(1>714)->  -GTCAAGTGGCAACTCCGTCAGCTCGTTAGAAAGATGATTTTGAGAACCTCTGAGGAAAC
                           _____
                           -GTCAAGTGGCAACTCCGTCAGCTCGTTAGAAAGATGATTTTGAGAACCTCTGAGGAAAC


                         310       320       330       340       350       360
                    ....|....|....|....|....|....|....|....|....|....|....|....|
HTPAN08P185FP14(1>338) <-  CATTTCTACAGTTCAAGRAAAGCAACCMAATATTTCTCCCCTAGTGAGAGAAAGAGGTCC
HTPAN08P185FP08(1>388) <-  CATTTCTACAGTTCAAGAAAAGCAACAAAATATTTCTCCCCTAGTGAGAGAAAGAGGTCC
htpan08 185bporf(1>714)->  CATTTCTACAGTTCAAGAAAAGCAACAAAATATTTCTCCCCTAGTGAGAGAAAGAGGTCC
                           _____
                           CATTTCTACAGTTCAAGAAAAGCAACAAAATATTTCTCCCCTAGTGAGAGAAAGAGGTCC


                         370       380       390       400       410       420
                    ....|....|....|....|....|....|....|....|....|....|....|....|
HTPAN08P185FP14(1>338) <-  TCAGAGAGTAGCAGCTCACATAACTGGGACCAGAGGGAGAAGCAACACATTSTCTTCTCC
HTPAN08P185FP08(1>388) <-  TCAGAGAGTAGCACCTCACATAACTGGGACCAGAGGAAGAAGCAACACATTGTCTTCTCC
htpan08 185bporf(1>714)->  TCAGAGAGTAGCAGCTCACATAACTGGGACCAGAGGAAGAAGCAACACATTGTCTTCTCC
                           _____
                           TCAGAGAGTAGCAGCTCACATAACTGGGACCAGAGGAAGAAGCAACACATTGTCTTCTCC
```

117

```
                                430       440       450       460       470       480
                              ....|....|....|....|....|....|....|....|....|....|....|....|
HTPAN08P185FP14(1>338) <-     AMACTCCAAGAATG
HTPAN08P185FP08(1>388) <-     AAACTCCAAGAATGAAAAGGCTCTGGRCCGCMAAATAAACTCCTGCGAATCATCAAGGAG
htpan08 185bporf(1>714)->     AAACTCCAAGAATGAAAAGGCTCTGGGCCGCAAAATAAACTCCTGGGAATCATCAAGGAG
                              AAACTCCAAGAATGAAAAGGCTCTGGGCCGCAAAATAAACTCCTGCGAATCATCAAGGAG


                                490       500       510       520       530       540
                              ....|....|....|....|....|....|....|....|....|....|....|....|
HTPAN08P185FP08(1>388) <-     TGG-CAT
htpan08 185bporf(1>714)->     TGGGCATTCATTCCTGAGCAACTTGCACTTGAGGAATGGTGAACTGGTCATCCATGAAAA
HTPAN08P185RP05(1>391) ->                         AAGAGGAATGGTGACCTGGTCATCCATGAAAA ...
                              TGG-CATTCATTCCTGAGCAACTTGCACAAGAGGAATGGTGAACTGGTCATCCATGAAAA


                                550       560       570       580       590       600
                              ....|....|....|....|....|....|....|....|....|....|....|....|
htpan08 185bporf(1>714)->     AGGGTTTTACTACATCTATTCCCAAACATACTTTCGATTTCAGGAGGAAATAAAAGAAAA
HTPAN08P185RP05(1>391) ->     AGGGTTTTACTACATCTATTCCCAAACATACTTTCGATTTCAGGAGGAAATAAAAGAAAA
HTPAN08P185FP17(1>259) ->                                                                A
                              AGGGTTTTACTACATCTATTCCCAAACATACTTTCGATTTCAGGAGGAAATAAAAGAAAA


                                610       620       630       640       650       660
                              ....|....|....|....|....|....|....|....|....|....|....|....|
htpan08 185bporf(1>714)->     CACAAAGAACGACAAACAAATGGTCCAATATATTTACAAATACACAAGTTATCCTGACCC
HTPAN08P185RP05(1>391) ->     CACAAAGAACGACAAACAAATGGYCCAATATATTTACAAATACACAAGTTATCCTGACCC
HTPAN08P185FP17(1>259) ->     CACAAGGAACGACACCCAN-TGGTCCAATATATTTACAAATACACAAGTTATCCTGACCC
                              CACAAAGAACGACAAACAAATGGTCCAATATATTTACAAATACACAAGTTATCCTGACCC


                                670       680       690       700       710       720
                              ....|....|....|....|....|....|....|....|....|....|....|....|
htpan08 185bporf(1>714)->     TATATTGTTGATGAAAAGTGCTAGAAATAGTTGTTGGTCTAAAGATGCAGAATATGGACT
HTPAN08P185RP05(1>391) ->     TATATTGTTGATGAAAAGTGCTAGAAATAGTTGTTGGTCTAAAGATGCAGAATATGGACT
HTPAN08P185FP17(1>259) ->     TATATTGTGGATGAAAAGTGCTAGAAATAGTKGTTGGTCTAAAGATGCAGAATATGGACT
                              TATATTGTTGATGAAAAGTGCTAGAAATAGTTGTTGGTCTAAAGATGCAGAATATGGACT


                                730       740       750       760       770       780
                              ....|....|....|....|....|....|....|....|....|....|....|....|
htpan08 185bporf(1>714)->     CTATTCCATCTATCAAGGGGGAATATTTGAGCTTAAGGAAAATGACAGAATTTTTGTTTC
HTPAN08P185RP05(1>391) ->     CTATTCCATCTATCARGGGGGAATATTTGAGCTTAAGGAAAATGACAGAATTTKTGTTTC
HTPAN08P185FP17(1>259) ->     CTATYCCATCTATCAAGGGGGAATWTTKGAGCTTAAGGAAAATGACAGAATTTTTGGTTTC
HTPAN08P185RP06(1>271) ->                                                               TC
                              CTATTCCATCTATCAAGGGGGAATATTTGAGCTTAAGGAAAATGACAGAATTTTTGTTTC


                                790       800       810       820       830       840
                              ....|....|....|....|....|....|....|....|....|....|....|....|
htpan08 185bporf(1>714)->     TGTAACAAATGAGCACTTGATAGACATGGACCATGAAGCCAGTTTTTTCGGGGCCTTTTT
HTPAN08P185RP05(1>391) ->     TGTAACAAATGAGCACTTGATAGACATGGACCATGAAGCCAGTTTTTTCGGGGCCTTTTT
HTPAN08P185FP17(1>259) ->     TGTAACAAATGAGCACTTGATAGACATGGACCATGAAGCCAGTTTTTYCGGGGCCTTTTT
HTPAN08P185RP06(1>271) ->     TGTAACAAATGAGCACTTGATAGACATGGACCATGAAGCCAGTTTTTTCGGGGCCTTTTT
                              TGTAACAAATGAGCACTTGATAGACATGGACCATGAAGCCAGTTTTTTCGGGGCCTTTTT
```

118

```
                         850       860       870       880       890       900
                    ....|....|....|....|....|....|....|....|....|....|....|....|
htpan08 185bporf(1>714)->  AGTTGGCTAA
HTPAN08P185RP05(1>391) ->  AGTTGGCTAAGCTCTAGATWCGCKCTTWWGGYTCCATCCCCRGAGATSATGTGCTCCAS
HTPAN08P185FP17(1>259) ->  AGTTGGYTAAGCTCTAGAT
HTPAN08P185RP06(1>271) ->  AGTTGGCTAAGCTCTAGATWCSCTCTWT-GGTTCCAT-CCCAGAGATCATRTGCTCCATW
                           AGTTGGCTAAGCTCTAGATACGCTCTTT-GGTTCCAT-CCCAGAGATCATGTGCTCCATA


                         910       920       930       940       950       960
                    ....|....|....|....|....|....|....|....|....|....|....|....|
HTPAN08P185RP06(1>271) ->  GGTGRGATTGGTYRTYCCTCAACTGGAGTTGAGAGWTATTGGTGACCCCATTGGYGAAGW
                           GGTGAGATTGGTCATCCCTCAACTGGAGTTGAGAGATATTGGTGACCCCATTGGCGAAGA


                         970       980       990       1000      1010      1020
                    ....|....|....|....|....|....|....|....|....|....|....|....|
HTPAN08P185RP06(1>271) ->  GAGTGTKAAYAGCCCCTGCTGGGAARYCAWGTTGAACYTCMGTCAGCWCGTTAGMAAGAT
                           GAGTGTGAACAGCCCCTGCTGGGAAACCAAGTTGAACCTCAGTCAGCACGTTAGAAAGAT


                         1030      1040      1050
                    ....|....|....|....|....|....|....|.
HTPAN08P185RP06(1>271) ->  SATTTGGATACMCTCTGTGGAACMCATTCAT
                           CATTTGGATACACTCTGTGGAACACATTCAT
```

119

```
                          10        20        30        40        50        60
                 ....|....|....|....|....|....|....|....|....|....|....|....|
HTPAN08PA51RP50(1>355)->  CACTCGCAAATAATAAGTATTTTACTGTTTTCGTAACAGTGTGGTAATAAAAAAAACCTAT
HTPAN08PA51FP16(1>238)<-                                             ACNCNAACCTAT
                          CACTCGCAAATAATAAGTATTTTACTGTTTTCGTAACAGTGTGGTAATAAAAAAAACCTAT


                          70        80        90        100       110       120
                 ....|....|....|....|....|....|....|....|....|....|....|....|
HTPAN08PA51RP50(1>355)->  AAATATTCCGGATTATTCATACCGCCCCACCATCGGGCGCGGATCCATCATGGNTATGAT
HTPAN08PA51FP16(1>238)<-  ARATATTCCGGATTATTCATACCGTCCCACCATCGGGCGCGGATCCATCATGTCTATGAT
htpan08orf(1>846)      ->                                              ATGGCTATGAT
                          AAATATTCCGGATTATTCATACCGCCCCACCATCGGGCGCGGATCCATCATGGCTATGAT


                          130       140       150       160       170       180
                 ....|....|....|....|....|....|....|....|....|....|....|....|
HTPAN08PA51RP50(1>355)->  GGAGGTCCAGGGGGGACCCAGCCTGGGACAGACCTGCGTGCTGATCGTGATCTTCACAGT
HTPAN08PA51FP16(1>238)<-  GGAGGTCCAGGGGGGACCCAGCCTGGGACAGACCTGCGTGCTGATCGTGATCTTCACAGT
htpan08orf(1>846)      ->  GGAGGTCCAGGGGGGACCCAGCCTGGGACAGACCTGCGTGCTGATCGTGATCTTCACAGT
HTPAN08PA51FP14(1>416)<-                       CCTGCGTGCTGATCGTGATCTTCACAGT
                          GGAGGTCCAGGGGGGACCCAGCCTGGGACAGACCTGCGTGCTGATCGTGATCTTCACAGT


                          190       200       210       220       230       240
                 ....|....|....|....|....|....|....|....|....|....|....|....|
HTPAN08PA51RP50(1>355)->  GCTCCTGNAGTCTCTCTGTGTGGNTGTAACTTACGTGTACTTTACCAACGAGCTGAAGSA
HTPAN08PA51FP16(1>238)<-  GCTCCTGCAGTCTCTCTGTGTGGCTGTAACTTACGTGTACTTTACCAACGAGCTGAAGCA
htpan08orf(1>846)      ->  GCTCCTGCAGTCTCTCTGTGTGGCTGTAACTTACGTGTACTTTACCAACGAGCTGAAGCA
HTPAN08PA51FP14(1>416)<-  GCTCCTGCAGTCTCTCTGTGTGGCTGTAACTTACGTGTACTTTACCAACGAGCTGAAGCA
HTPAN08PA51FP08(1>389)<-                                            AACGAGCTGAAGCA
HTPAN08PA51RP12(1>371)->                                          CCAACGAGCTGAAGCA
                          GCTCCTGCAGTCTCTCTGTGTGGCTGTAACTTACGTGTACTTTACCAACGAGCTGAAGCA


                          250       260       270       280       290       300
                 ....|....|....|....|....|....|....|....|....|....|....|....|
HTPAN08PA51RP50(1>355)->  GATGSAGGAC-AARTW-CTCCAAAAGTGGCATTGSTTGTTTCTTAAAAGAAGATGACAGT
HTPAN08PA51FP16(1>238)<-  GATGCAGGAC-AAGTA-CTCCMMCAGTGACATTGCTTGTTTCTT
htpan08orf(1>846)      ->  GATGCAGGAC-AAGTA-CTCCAAAAGTGGCATTGCTTGTTTCTTAAAAGAAGATGACAGT
HTPAN08PA51FP14(1>416)<-  GATGCAGGAC-AAGTA-CTCCMMAAGTGGCATTGCTTGTTTCTTRARAGAAGATGACAGT
HTPAN08PA51FP08(1>389)<-  GATGCAGGACCAAGTACCTCCAAAAGTGGCATTGCTTGTTTCGTAAAAGAAGATGACAGT
HTPAN08PA51RP12(1>371)->  GATGCAGGAC-AAGTA-CTCCAAAAGTGGCATTGCTTGTTTCTTAAAAGAAGATGACAGT
HTPAN08PA51RP10(1>339)->                                       GTTTGTTTCTTAAAAGAAGATGACAGT
                          GATGCAGGAC-AAGTA-CTCCAAAAGTGGCATTGCTTGTTTCTTAAAAGAAGATGACAGT


                          310       320       330       340       350       360
                 ....|....|....|....|....|....|....|....|....|....|....|....|
HTPAN08PA51RP50(1>355)->  TATTGGGACCCCAATGACGAAGAGAGTATGAACAGCCCCTGGTGGCAAGTCAAGTGG
htpan08orf(1>846)      ->  TATTGGGACCCCAATGACGAAGAGAGTATGAACAGCCCCTGCTGGCAAGTCAAGTGGCAA
HTPAN08PA51FP14(1>416)<-  TATTGGGACCCCAATGACGAAGAGAGTATGAACAGCCCCTGCTGGCAAGTCAAGTGGCAA
HTPAN08PA51FP08(1>389)<-  TATTGGGACCCCAATGACGAAGAGAGTATGAACAGCCCCTGCTGGCAAGTCAAGTGGCAA
HTPAN08PA51RP12(1>371)->  TATTGGGACCCCAATGACGAAGAGAGTATGAACAGCCCCTGCTGGCAAGTCAAGTGGCAA
HTPAN08PA51RP10(1>339)->  TATTGGGACCCCAATGACGAAGAGAGTATGAACAGCCCCTGCTGGCAAGTCAAGTGGCAA
                          TATTGGGACCCCAATGACGAAGAGAGTATGAACAGCCCCTGCTGGCAAGTCAAGTGGCAA
```

120

```
                                   370       380       390       400       410       420
                              ...|....|....|....|....|....|....|....|....|....|....|....|
htpan08orf(1>846)         ->  CTCCGTCAGCTCGTTAGAAAGATGATTTTGAGAACCTCTGAGGAAACCATTTCTACAGTT
HTPAN08PA51FP14(1>416)<-      CTCCGTCAGCTCGTTAGAAAGATGATTTTGAGAACCTCTGAGGAAACCATTTCTACAGTT
HTPAN08PA51FP08(1>389)<-      CTCCGTCAGMTCGTTAGAAAGATGATTTTGAGAACCTCTGAGGAAACCATTTCTACAGTT
HTPAN08PA51RP12(1>371)->      CTCCGTCAGCTCGTTAGAAAGATGATTKTGRGAACCTCTGAGGAAACCATTTCTACAGYT
HTPAN08PA51RP10(1>339)->      CTCCGTCAGCTCGTTAGAAAGATGATTTGGAGAACCTCTGAGGAAACCATTTCTACAGTT
                              CTCCGTCAGCTCGTTAGAAAGATGATTTTGAGAACCTCTGAGGAAACCATTTCTACAGTT

                                   430       440       450       460       470       480
                              ...|....|....|....|....|....|....|....|....|....|....|....|
htpan08orf(1>846)         ->  CAAGAAAAGCAACAAAATATTTCTCCCCTAGTGAGAGAAAGAGGTCCTCAGAGAGTAGCA
HTPAN08PA51FP14(1>416)<-      CAAGAAAAGCAACMAAATATTTCTCCCCTAGTGAGAGAAAGAGGTCCTCAGAGAGTAGCA
HTPAN08PA51FP08(1>389)<-      CAAGAAAAGCAACAAAATATTTCTCCCCTAGTGAGAGAAAGAGGTCCTCAGAGAGTAGCA
HTPAN08PA51RP12(1>371)->      CAAGAAAAGCAACAAAATATTTCTCCCCTAGTGAGAGAAAGAGGTCCTCAGAGAGTAGCA
HTPAN08PA51RP10(1>339)->      CAAGAAAAGCAACAAAATTATTTCTCCCCTAGTGAGAGAAAGAGGTCCTCAGAGAGTAGCA
                              CAAGAAAAGCAACAAAATATTTCTCCCCTAGTGAGAGAAAGAGGTCCTCAGAGAGTAGCA

                                   490       500       510       520       530       540
                              ...|....|....|....|....|....|....|....|....|....|....|....|
htpan08orf(1>846)         ->  GCTCACATAACTGGGACCAGAGGAAGAAGCAACACATTGTCTTCTCCAAACTCCAAGAAT
HTPAN08PA51FP14(1>416)<-      GCTCACATAACTGGGACCAGAGGAAGAAGCAACACATTGTCTTCTCCAAACTCCAAGAAT
HTPAN08PA51FP08(1>389)<-      GCTCACATAACTGGGACCAGAGGAAGAAGCAACACATTGTCTTCTCCAAACTCCAAGAAT
HTPAN08PA51RP12(1>371)->      GCTCACATAACTGGGACCAGAGGAAGAAGCAACACATTGTCTTCTCCAAACTCCAAGAAT
HTPAN08PA51RP10(1>339)->      GCTCACATAACTGGGACCAGAGGAAGAAGMAACACATTGTCTTCTCCAAACTCCAAGAAT
                              GCTCACATAACTGGGACCAGAGGAAGAAGCAACACATTGTCTTCTCCAAACTCCAAGAAT

                                   550       560       570       580       590       600
                              ...|....|....|....|....|....|....|....|....|....|....|....|
htpan08orf(1>846)         ->  GAAAAGGCTCTGGGCCGCAAAATAAACTCCTGGGAATCATCAAGGAGTGGGCATTCATTC
HTPAN08PA51FP14(1>416)<-      GAGAAGNCTCTGGGCCGC
HTPAN08PA51FP08(1>389)<-      GAAAAGGCTCTGGGCCGCAAAATAAACTCCTGGGAATCATCAAGGAGTGGGCA
HTPAN08PA51RP12(1>371)->      GAAAAGGCTCTKGGCCSCAAAATAAACTCCTGGGAATCATCAAGGAGTGGGCA
HTPAN08PA51RP10(1>339)->      GAAAAGGSTCTGGGCCGCAAAATAAACTCCTGGGAATCATCAAGGAGTGGGSATTCATTC
                              GAAAAGGCTCTGGGCCGCAAAATAAACTCCTGGGAATCATCAAGGAGTGGGCATTCATTC

                                   610       620       630       640       650       660
                              ...|....|....|....|....|....|....|....|....|....|....|....|
htpan08orf(1>846)         ->  CTGAGCAACTTGCACTTGAGGAATGGTGAACTGGTCATCCATGAAAAAGGGTTTTACTAC
HTPAN08PA51RP10(1>339)->      CTGAGCAACTTG
HTPAN08PA51RP05(1>329)->                        ATGGTGAACTGGTCATCCATGAAAAAGGGTTTTACTAC
                              CTGAGCAACTTGCACTTGAGGAATGGTGAACTGGTCATCCATGAAAAAGGGTTTTACTAC

                                   670       680       690       700       710       720
                              ...|....|....|....|....|....|....|....|....|....|....|....|
htpan08orf(1>846)         ->  ATCTATTCCCAAACATACTTTCGATTTCAGGAGGAAATAAAAGAAAACACAAAGAACGAC
HTPAN08PA51RP05(1>329)->      ATCTATTCCCAAACATACTTTCGATTTCAGGAGGAAATAAAAGAAAACACAAAGAACGAC
HTPAN08PA51FP17(1>223)->                                               ACAAAGAACGAG
                              ATCTATTCCCAAACATACTTTCGATTTCAGGAGGAAATAAAAGAAAACACAAAGAACGAC
```

121

```
                  730       740       750       760       770       780
                  ....|....|....|....|....|....|....|....|....|....|....|....|
htpan08orf(1>846)      ->  AAACAAATGGTCCAATATATTTACAAATACACAAGTTATCCTGACCCTATATTGTTGATG
HTPAN08PA51RP05(1>329)->  AAACAAATGGYCCAATATATTTACAAATACACAAGTTATCCTGACCCTATATTGTTGATG
HTPAN08PA51FP17(1>223)->  ACCCACCTGAACCAATATTTTTACAAATACACAAGTTATCCTGACCCTATATTGTGGATG
                          AAACAAATGGTCCAATATATTTACAAATACACAAGTTATCCTGACCCTATATTGTTGATG


                  790       800       810       820       830       840
                  ....|....|....|....|....|....|....|....|....|....|....|....|
htpan08orf(1>846)      ->  AAAAGTGCTAGAAATAGTTGTTGGTCTAAAGATGCAGAATATGGACTCTATTCCATCTAT
HTPAN08PA51RP05(1>329)->  AAAAGTGCTAGAAATAGTTGTTGGTCTAAAGATGCAGAATATGGACTCTATTCCATCTAT
HTPAN08PA51FP17(1>223)->  AAAAGTGCTAGAAATAGTKGTKGGYCTAAAGATGMAGNCCNNGGACTCTATTCCATCTAT
                          AAAAGTGCTAGAAATAGTTGTTGGTCTAAAGATGCAGAATATGGACTCTATTCCATCTAT


                  850       860       870       880       890       900
                  ....|....|....|....|....|....|....|....|....|....|....|....|
htpan08orf(1>846)      ->  CAAGGGGGAATATTTGAGCTTAAGGAAAATGACAGAATTTTTGTTTCTGTAACAAATGAG
HTPAN08PA51RP05(1>329)->  CAAGGGGGAATATTTGAGCTTAAGGAAAATGACAGAATTTNTGTTTCTGTAACAAATGAG
HTPAN08PA51FP17(1>223)->  CAAGGGGGAATATTGGAGCTTAAGGAAAATGACAGAATTTNGGTTTCTGTAACAAATGAG
HTPAN08PA51RP06(1>219)->                                              TTTCTGTAACAAATGAG
                          CAAGGGGGAATATTTGAGCTTAAGGAAAATGACAGAATTTTTGTTTCTGTAACAAATGAG


                  910       920       930       940       950       960
                  ....|....|....|....|....|....|....|....|....|....|....|....|
htpan08orf(1>846)      ->  CACTTGATAGACATGG-ACCATGAAGCCAGTTTTTTCGGGGCCTTTTTAGTTGGCTAA
HTPAN08PA51RP05(1>329)->  CACTTGATAGACATGGCACCGCGAAGCCA
HTPAN08PA51FP17(1>223)->  CACTTGATAGACATGG-ACCGNGAAGCCAG
HTPAN08PA51RP06(1>219)->  CACTTGATAGACATGG-ACCGTGAAGCCAGTTTTTTCGGGGCCTTTTTAGTTGGCTAAGC
                          CACTTGATAGACATGG-ACCGTGAAGCCAGTTTTTTCGGGGCCTTTTTAGTTGGCTAAGC


                  970       980       990       1000      1010      1020
                  ....|....|....|....|....|....|....|....|....|....|....|....|
HTPAN08PA51RP06(1>219)->  TCTAGAAAAGATCTAAGGTACCGATCCAGACATGATAAGATACATTGATGAGTTNGGACA
                          TCTAGAAAAGATCTAAGGTACCGATCCAGACATGATAAGATACATTGATGAGTTXGGACA


                  1030      1040      1050      1060      1070      1080
                  ....|....|....|....|....|....|....|....|....|....|....|....|
HTPAN08PA51RP06(1>219)->  AACCACAACTAGAATGCAGNGAAAAAAATGCTTTATTTGTGAAATTNGNGATGCTATTGC
                          AACCACAACTAGAATGCAGXGAAAAAAATGCTTTATTTGTGAAATTXGXGATGCTATTGC


                  1090
                  ....|....|....|....|....
HTPAN08PA51RP06(1>219)->  TTTATTTGGAACCATTAT
                          TTTATTTGGAACCATTAT
```

122

— FAS —

```
ATGGCTATGATGGAGGTCCAGGGGGGGACCCAGCCTGGGACAGACCTGCGTGCTGATCGTGATCTTCACAG
+----+----+----+----+----+----+----+----+----+----+----+----+----+----+ 70
TACCGATACTACCTCCAGGTCCCCCCCTGGGTCGGACCCTGTCTGGACGCACGACTAGCACTAGAAGTGTC

 M  A  M  M  E  V  Q  G  G  P  S  L  G  Q  T  C  V  L  I  V  I  F  T
 W  L  .  W  R  S  R  G  D  P  A  W  D  R  P  A  C  .  S  .  S  S  Q
 N  G  Y  D  G  G  P  G  G  T  Q  P  G  T  D  L  R  A  D  R  D  L  H  S
 +----+----+----+----+----+----+----+----+----+----+----+----+----+----+
```

```
TGCTCCTGCAGTCTCTCTGTGTGGCTGTAACTTACGTGTACTTTACCAACGAGCTGAAGCAGATGCAGGA
+----+----+----+----+----+----+----+----+----+----+----+----+----+----+ 140
ACGAGGACGTCAGAGAGACACACCGACATTGAATGCACATGAAATGGTTGCTCGACTTCGTCTACGTCCT

 V  L  L  Q  S  L  C  V  A  V  T  Y  V  Y  F  T  N  E  L  K  Q  M  Q  D
 C  S  C  S  L  S  V  W  L  .  L  T  C  T  L  P  T  S  .  S  R  C  R
 A  P  A  V  S  L  C  G  C  N  L  R  V  L  Y  Q  R  A  E  A  D  A  G
 +----+----+----+----+----+----+----+----+----+----+----+----+----+----+
```

```
CAAGTACTCCAAAAGTGGCATTGCTTGTTTCTTAAAAGAAGATGACAGTTATTGGGACCCCAATGACGAA
+----+----+----+----+----+----+----+----+----+----+----+----+----+----+ 210
GTTCATGAGGTTTTCACCGTAACGAACAAAGAATTTTCTTCTACTGTCAATAACCCTGGGGTTACTGCTT

 K  Y  S  K  S  G  I  A  C  F  L  K  E  D  D  S  Y  W  D  P  N  D  E
 T  S  T  P  K  V  A  L  L  V  S  .  K  K  M  T  V  I  G  T  P  M  T  K
 Q  V  L  Q  K  W  H  C  L  F  L  K  R  R  .  Q  L  L  G  P  Q  .  R
 +----+----+----+----+----+----+----+----+----+----+----+----+----+----+
```

```
GAGAGTATGAACAGCCCCTGCTGGCAAGTCAAGTGGCAACTCCGTCAGCTCGTTAGAAAGATGATTTTGA
+----+----+----+----+----+----+----+----+----+----+----+----+----+----+ 280
CTCTCATACTTGTCGGGGACGACCGTTCAGTTCACCGTTGAGGCAGTCGAGCAATCTTTCTACTAAAACT

 E  S  M  N  S  P  C  W  Q  V  K  W  Q  L  R  Q  L  V  R  K  M  I  L
 R  V  .  T  A  P  A  G  K  S  S  G  N  S  V  S  S  L  E  R  .  F  .
 R  E  Y  E  Q  P  L  L  A  S  Q  V  A  T  P  S  A  R  .  K  D  D  F  E  .
 +----+----+----+----+----+----+----+----+----+----+----+----+----+----+
```

```
GAACCTCTGAGGAAACCATTTCTACAGTTCAAGAAAAGCAACAAAATATTTCTCCCCTAGTGAGAGAAAG
+----+----+----+----+----+----+----+----+----+----+----+----+----+----+ 350
CTTGGAGACTCCTTTGGTAAAGATGTCAAGTTCTTTTCGTTGTTTTATAAAGAGGGGATCACTCTCTTTC

 R  T  S  E  E  T  I  S  T  V  Q  E  K  Q  Q  N  I  S  P  L  V  R  E  R
 E  P  L  R  K  P  F  L  Q  F  K  K  S  N  K  I  F  L  P  .  .  E  K
 N  L  .  G  N  H  F  Y  S  S  R  K  A  T  K  Y  F  S  P  S  E  R  K
 +----+----+----+----+----+----+----+----+----+----+----+----+----+----+
```

```
AGGTCCTCAGAGAGTAGCAGCTCACATAACTGGGACCAGAGGAAGAAGCAACACATTGTCTTCTCCAAAC
+----+----+----+----+----+----+----+----+----+----+----+----+----+----+ 420
TCCAGGAGTCTCTCATCGTCGAGTGTATTGACCCTGGTCTCCTTCTTCGTTGTGTAACAGAAGAGGTTTG

 G  P  Q  R  V  A  A  H  I  T  G  T  R  G  R  S  N  T  L  S  S  P  N
 E  V  L  R  E  .  Q  L  T  .  L  G  P  E  E  E  A  T  H  C  L  L  Q  T  .
 R  S  S  E  S  S  S  S  H  N  W  D  Q  R  K  K  Q  H  I  V  F  S  K
 +----+----+----+----+----+----+----+----+----+----+----+----+----+----+
```

123

```
TCCAAGAATGAAAAGGCTCTGGGCCGCAAAATAAACTCCTGGGAATCATCAAGGAGTGGGCATTCATTCC
+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+ 490
AGGTTCTTACTTTTCCGAGACCCGGCGTTTTATTTGAGGACCCTTAGTAGTTCCTCACCCGTAAGTAAGG

   S  K  N  E  K  A  L  G  R  K  I  N  S  W  E  S  S  R  S  G  H  S  F
    P  R  M  K  R  L  W  A  A  K  .  T  P  G  N  H  Q  G  V  G  I  H  S
  L  Q  E  .  K  G  S  G  P  Q  N  K  L  L  G  I  I  K  E  W  A  F  I  P


TGAGCAACTTGCACTTGAGGAATGGTGAACTGGTCATCCATGAAAAAGGGTTTTACTACATCTATTCCCA
+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+ 560
ACTCGTTGAACGTGAACTCCTTACCACTTGACCAGTAGGTACTTTTTCCCAAAATGATGTAGATAAGGGT

   L  S  N  L  H  L  R  N  G  E  L  V  I  H  E  K  G  F  Y  Y  I  Y  S  Q
    .  A  T  C  T  .  G  M  V  N  W  S  S  M  K  K  G  F  T  T  S  I  P
     E  Q  L  A  L  E  E  W  .  T  G  H  P  .  K  R  V  L  L  H  L  F  P


AACATACTTTCGATTTCAGGAGGAAATAAAAGAAAACACAAAGAACGACAAACAAATGGTCCAATATATT
+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+ 630
TTGTATGAAAGCTAAAGTCCTCCTTTATTTTCTTTTGTGTTTCTTGCTGTTTGTTTACCAGGTTATATAA

    T  Y  F  R  F  Q  E  E  I  K  E  N  T  K  N  D  K  Q  M  V  Q  Y  I
  K  H  T  F  D  F  R  R  K  .  K  K  T  Q  R  T  T  N  K  W  S  N  I  F
   N  I  L  S  I  S  G  G  N  K  R  K  H  K  E  R  Q  T  N  G  P  I  Y


TACAAATACACAAGTTATCCTGACCCTATATTGTTGATGAAAAGTGCTAGAAATAGTTGTTGGTCTAAAG
+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+ 700
ATGTTTATGTGTTCAATAGGACTGGGATATAACAACTACTTTTCACGATCTTTATCAACAACCAGATTTC

   Y  K  Y  T  S  Y  P  D  P  I  L  L  M  K  S  A  R  N  S  C  W  S  K
    T  N  T  Q  V  I  L  T  L  Y  C  .  .  .  K  V  L  E  I  V  V  G  L  K
   L  Q  I  H  K  L  S  .  P  Y  I  V  D  E  K  C  .  K  .  L  L  V  .  R


ATGCAGAATATGGACTCTATTCCATCTATCAAGGGGGAATATTTGAGCTTAAGGAAAATGACAGAATTTT
+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+ 770
TACGTCTTATACCTGAGATAAGGTAGATAGTTCCCCCTTATAAACTCGAATTCCTTTTACTGTCTTAAAA

   D  A  E  Y  G  L  Y  S  I  Y  Q  G  G  I  F  E  L  K  E  N  D  R  I  F
    M  Q  N  M  D  S  I  P  S  I  K  G  E  Y  L  S  L  R  K  M  T  E  F
     C  R  I  W  T  L  F  H  L  S  R  G  N  I  .  A  .  G  K  .  Q  N  F


TGTTTCTGTAACAAATGAGCACTTGATAGACATGGACCATGAAGCCAGTTTTTTCGGGGCCTTTTTAGTT
+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+ 840
ACAAAGACATTGTTTACTCGTGAACTATCTGTACCTGGTACTTCGGTCAAAAAAGCCCCGGAAAAATCAA

   V  S  V  T  N  E  H  L  I  D  M  D  H  E  A  S  F  F  G  A  F  L  V
    L  F  L  .  Q  M  S  T  .  .  T  W  T  M  K  P  V  F  S  G  P  F  .  L
     C  F  C  N  K  .  A  L  D  R  H  G  P  .  S  Q  F  F  R  G  L  F  S
```

124

```
GGCTAA
━━━━━➤ 846
CCGATT

  G   . .
   A  K
W  L
━━━━━➤
```

HTPANO8SO4 5lbp +PDI?

in 6M Gn HCl - ELUTED OVER NiSO4 Column

43.0 Kda

29.1 Kda

18.8 Kda

16.5 KDa
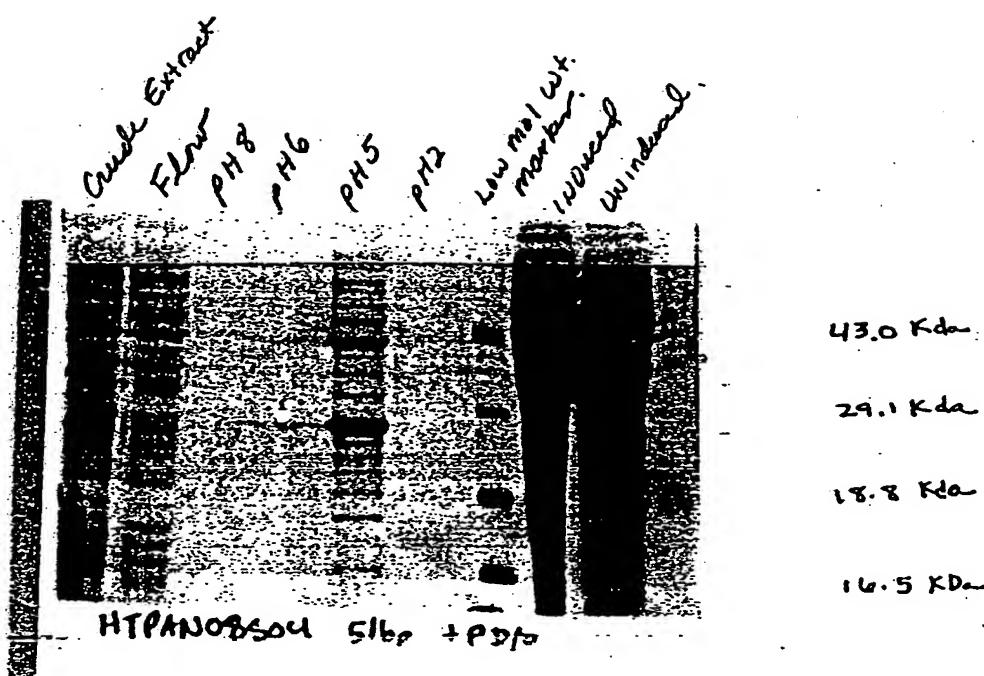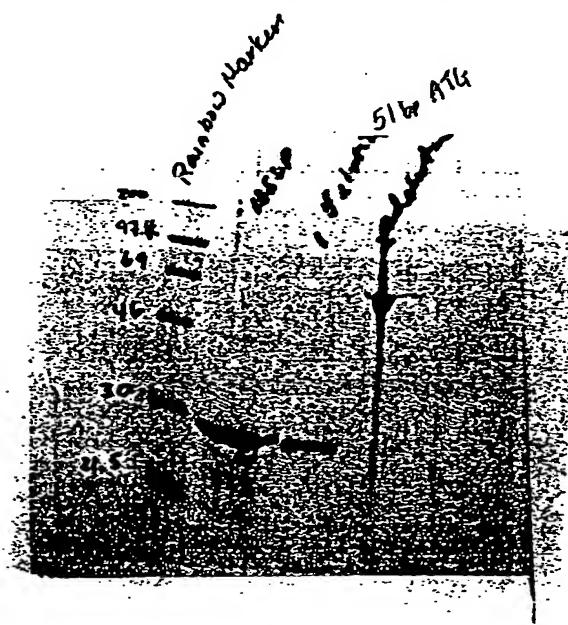
HTPANO8SO4 185bp ATG vs   HTPANO8SO4 5lbp ATG
PH5 elution   1st Elution & 2nd ELUTION IN Immidiol

The TNF Receptor Superfamily of Cellular and Viral Proteins: Activation, Costimulation, and Death

Minireview

Craig A. Smith, Terry Farrah,
and Raymond G. Goodwin
Departments of Biochemistry and Molecular Biology
Immunex Corporation
Seattle, Washington 98101

Tumor necrosis factor (TNF) seems always to have enjoyed a rather conspicuous visibility in biomedical research. With historical roots in the century-old phenomenon of bacterial-induced hemorrhagic necrosis of tumors, TNF—or, rather, its two homologous forms, TNFα and LTα (lymphotoxin, TNFβ)—were finally molecularly cloned in 1984, among the very first cytokines to be so unambiguously defined. Although TNFα and LTα, classically the respective products of activated macrophages and T cells, can indeed kill many transformed lines, these functionally similar and extraordinarily pleiotropic cytokines are today viewed as primary mediators of immune regulation and the inflammatory response, closely linked to the development of disease. The crucial involvment of TNF, for example, in septic shock, some autoimmune disorders, and graft-host disease is well established (see Beutler, 1992).

Since the cloning of two distinct but structurally homologous receptors for TNF, p75 and p55 (each of which binds both ligands), the past 3 years have witnessed the rapid emergence of two superfamilies, of which the TNFs and their receptors are only representatives (Farrah and Smith, 1992; Suda et al., 1993; Smith et al., 1993). To date, 12 receptors have been identified (Figure 1) with which we can associate some eight TNF-related cytokines (Figure 2). The distinctive but overlapping cellular responses their interactions produce clearly define developmental and regulatory networks involving cells of the lymphoid, hematopoetic, and other lineages. In this minireview we make no attempt to discuss individual members comprehensively and instead highlight emerging global characteristics that distinguish them from other cytokine families: structure, biological networks, and the intriguing ability of some members to induce cell death. A new face to the TNF system seems at hand.

The TNF Receptor Family Interacts with a Parallel Family of Ligands

The receptors, with two exceptions, are all type I membrane proteins with sequence homology (almost entirely) confined to the extracellular region. The exceptions, T2 and A53R, are poxvirus gene products that map to different genetic loci and have been shown to encode soluble, secreted forms of TNF receptors (Smith et al., 1991). These function to complex (and thereby inactivate) host-produced TNF. T2 is clearly an acquired form of the p75 cellular receptor, while A53R, since it binds only TNFα and shows much lower sequence homology, may represent a third TNF receptor. The extraordinary virulence of wild-type myxoma poxvirus, uniformly fatal to its host (rabbits), is reduced nearly 50% in recombinants differing only by an inactivated T2 gene (Upton et al., 1991). Interestingly,

an intact T2 gene is also conserved in the recently sequenced variola genome, the pathogen responsible for smallpox in humans (Shchelkunov et al., 1993).

The canonical motif of all these receptors is that of cysteine-rich pseudorepeats, each containing about six cysteines and 40 amino acids, although considerable variation in size and number is evident (e.g., CD30 and CD27). Soluble forms, released by proteolysis, for most of these receptors have been observed; one (4-1BB) is generated through alternative splicing (Goodwin et al., 1993). The cytoplasmic domains are rather small (46–221 residues) and generally lack sequence homology among themselves, suggesting major differences in signaling mechanisms. None possess sequences implying catalytic activity.

The ligands for CD30, CD27, CD40, 4-1BB, and Fas were identified and cloned not by protein sequencing, but through direct expression cloning strategies (Goodwin et al., 1993; Suda et al., 1993). This approach rested on the assumption that putative ligands would, like TNFα, exist in active surface forms identifiable by specific binding of soluble receptors (as immunoglobulin fusion chimerics). In fact, all ligands except LTα, which appears to be a secreted protein, reflect prototypic pro-TNFα architecture: type II membrane proteins, with the C-terminus extracellular, the N-terminus intracellular, and a single transmembrane element. Soluble (proteolytically released) forms of TNFα are well known, although reports have not yet established such alternative forms for other ligand members. Family-defining sequence homology (Figure 3) is restricted to ~150 residues in the C-terminal (receptor-
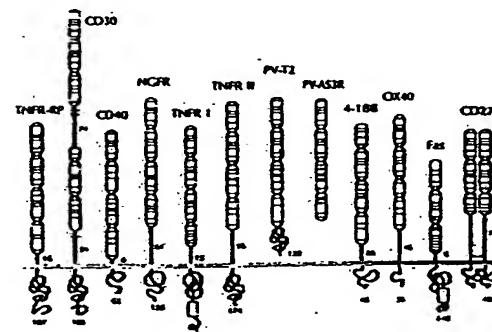
Figure 1. The TNF Receptor Superfamily

Homologous domains are shown as open boxes and cysteine residues by horizontal lines. Number of amino acids in the (nonhomologous) extracellular linker and cytoplasmic domains are indicated. Stippled boxes in the cytoplasmic regions represent death domains. TNFR-RP is a predicted family member encoded by a transcribed sequence from human chromosome 12p (Baens et al., 1993). OX40 is a rat T cell activation antigen with no reported cognate. In laboratory strains of vaccinia virus, the A53R open reading frame is interrupted by a premature termination codon (Goebel et al., 1990). See Goodwin et al. (1993) for original references.
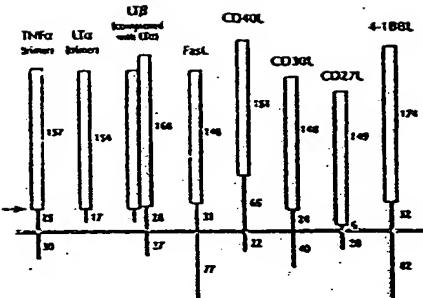
Figure 2. The TNF Family of Cytokines

The homologous C-terminal domains are indicated by open boxes. Extracellular and cytoplasmic domains, which lack sequence homology, are indicated by closed bars. The number of amino acids in each domain is shown. LTα is shown in both secreted and alternative membrane-associated forms, complexed with LTβ. The arrow indicates the proteolytic cleavage site in pro-TNFα that allows for the release of soluble form. Only TNFα, LTα, and LTβ have been shown to form oligomers.

Figure 4. Crystal Structure of Soluble p55 TNFR–LTα Complex
Reprinted from Figure 4 in Banner et al. (1993).

binding) region, which in soluble TNFα and LTα fold into a β-pleated sheet sandwich and trimerize (Eck et al., 1992; Jones et al., 1989). Sequence conservation is particularly high at protomer interfaces. It seems likely, therefore, that all ligands in this family adopt a similar tertiary structure and form oligomers.

A unifying picture of the prototypic interation between ligands and receptors has literally crystallized from a milestone X-ray diffraction study by Banner et al. (1993), who solved the structure of a human LTα-soluble p55 TNF receptor complex. This complex, containing the extracellular portions of three receptors bound to one LTα trimer, clearly establishes the pseudorepeat sequences in the receptor as true domains forming an elongated array that lies in the interfaces between each pair of the three ligand protomers (Figure 4). Roughly 80% of receptor–ligand contacts occur through domain 2, and each receptor contacts both protomers in the interface. Such a complex would bring receptor cytoplasmic domains into close apposition, presumably complementing binding sites for unknown signaling components, and is consistent with ligand-induced receptor cross-linking as the near universal activation mecha-

nism for growth factors. The novel feature here is that activation involves receptor trimerization; most cytokine families appear to induce dimerization, although by different schemes. Platelet-derived growth factor, for example, is a dimer (immunoglobulin family) whose receptor is a tyrosine kinase, while growth hormone, a member of the hematopoietin family, is a heterodivalent monomer (De Vos et al., 1992).

Many observations, however, suggest this disarmingly simple picture may need revisions. First, structural divergencies in other family members imply variations in interaction motifs. CD30, for example, contains six domains, not four, separated by a nonhomologous region of 74 residues, while CD27 contains three domains, one truncated, and appears to be a disulfide-linked dimer. Further, some evidence suggests that TNFα and LTα oligomers may be intrinsically polydisperse, consisting of homodimers, trimers, and tetramers (Schoenfeld et al., 1990).

Second, one ligand family member (LTβ), with no known biological activity, has been shown to form heterologous complexes with mature LTα (e.g. β2α1), serving to anchor
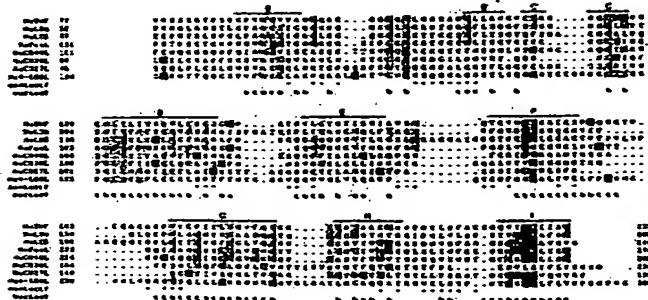
Figure 3. Sequence Homology in C-Terminal Domains of TNF Ligand Family

Alignment begins with N-terminus of soluble TNFα. Residues conserved in four or more members are stippled; cysteines are in closed boxes. Letters B–I indicate β strands in TNF tertiary structure. Asterisks indicate residues having p55 receptor contacts in crystal structure. Lowercase b indicates buried residues in the β-sheet interior; t, residues at TNF protomer–protomer interfaces.

the normally secreted LTα to the cell surface of T, B, and NK cells (Browning et al., 1993). Superficially, these ligands thus begin to resemble cassettes, whereby combinatorial arrangements could produce different oligomers with potentially altered receptor specificities, greatly increasing diversity of function. Such a mechanism in an entirely different family is reflected by the use of the platelet-derived growth factor A and B ligand subunits (A–A, A–B, and B–B dimers) to generate heterotypic and homotypic cross-linked dimers of the α and β receptors. Generic ligand–receptor interactions suggested by the crystal structure of LTα–p55, however, predict that mixed oligomers of LTα–LTβ would produce inactive (that is, ligand-bound but un-cross-linked) p55 (or p75) TNF receptor complexes. This suggests one function of LTβ is to inactivate LTα (with respect to TNF receptors) and implies the existence of a distinct receptor for LTβ that, when cross-linked, would generate novel signals. Heterologous complexes with still other family members could enormously increase the complexity of biological networks.

Third, there is no clear rationale for the redundancy built into the TNFα/LTα (p55/p75) system, nor is it clear how common such redundancies will be in other family members. These ligands display nearly identical biological activities and bind each receptor. Most cells, however, express variable levels of both receptors, even though heterologous receptor cross-links seem prohibited and each receptor can, on its own, transduce different signals (Pfeffer et al., 1993; Tartaglia et al., 1993). One implication is that functional cross-talk may exist between family members.

Fourth, the cytoplasmic domains of these ligands clearly serve important but unknown functions: they are nearly as conserved in sequence across species as extracellular regions, suggesting they carry binding sites for unidentified proteins. For example, we calculate the cytoplasmic domains of human and mouse CD40L are 82% identical; mouse and human TNFα, 86%; mouse and human CD30L, 61%. There is little homology among these domains in different ligands, however, arguing against conservation as a result of common biosynthetic or internalization mechanisms. Since direct cell–cell contact is a primary means of ligand–receptor interaction in this family, bipolar signaling may occur, blurring the distinction between receptor and ligand.

Finally, the low affinity nerve growth factor receptor (NGFR), while structurally a member of this family, binds a family of ligands (the neurotropins) structurally rather different than TNF. NGFR also interacts with the trk family of receptor tyrosine kinases, which show no homology to TNF receptors. Further, while the genomic architectures of CD40, both TNF receptors, and CD27 are rather similar, they appear quite different from the p75 NGFR. Thus, whether the (extracellular) structural homology of NGFR subunit reflects a functional interaction or even distant evolutionary relatedness between these two systems is unclear (Smith et al., 1993). Intriguingly, however, NGF has been shown to affect lymphocyte function. NGFRs are expressed at high levels on follicular dedritic cells in germinal centers, and TNF receptors are expressed on

glial cells of the nervous system, raising the possibility of functional interplay.

Biological Networks: Apoptosis, Necrosis, and Costimulation

Ligand family members can induce pleiotropic biological responses, including differentiation, proliferation, activation, or even cell death. It is clear, however, that T cell-mediated immunity, particularly contact dependent and antigen driven, provides one unifying theme. Without exception, all ligands as well as their receptors are T cell products (although not uniquely so). Both human PBT cells and CD4⁺ T cell clones show enhanced proliferation when treated with any family ligand in the presence of monoclonal antibodies to CD3 (Goodwin et al., 1993). Thus, autocrine T cell loops, largely mediated through cell–cell contact, are a common feature of the family. The observed variation in ligand induction kinetics is also consistent with different roles for these ligands in T cell activation (Smith et al., 1993; Beutler, 1992). As B cells are also capable of expressing receptors for CD30, CD40, TNFα, LTα, and CD27, for example, this family may contribute T cell help to B cells as well. TNFα and CD30L, however, are also abundantly expressed by activated macrophages, with receptors for the former expressed on nearly all vertebrate cells. Clearly, the dominant physiological networks are an evolving subject.

A consequence of the type II membrane protein architecture of these ligands, particularly on T and B cells, is the cell–cell contact nature of the interaction: it helps ensure ligand expression is antigen dependent and demands that signals generated by TNF family ligands in target cells are productively coordinated with accessory signals generated by other cognate pairs (e.g., cytokine–receptors, CD80–CD28, adhesion molecules such as CD58–CD2). The essence of signaling in this family is therefore one of costimulation. Soluble forms of TNFα (or perhaps CD30L) produced by macrophage may serve to extend the range of activities and provide flexibility to the immune response (Browning et al., 1993; Smith et al., 1993).

The biological function of CD40–CD40L provides a particularly clear example of costimulatory function. Almost exclusively the product of activated CD4⁺ T cells, CD40L provides essential signals to purified B cells, costimulated with interleukin-4, to undergo immunoglobulin isotype switching and to secrete mature immunoglobulin. Confirmation of this in vitro picture comes from studies of patients carrying mutations in the X-linked CD40L gene: patients show normal numbers of B cells, but a virtual absence of immunoglobulin isotypes other than immunoglobulin M and an inability to mount an antigen-specific antibody response, with concomitant susceptibility to opportunistic infections (Callard et al., 1993).

The TNFα/LTα (p55/p75) system is more complex. Transgenic mice deleted of the p55 TNF receptor illuminate the fundamental importance of TNF and this receptor while illustrating the difficulty in unraveling networks in such a pleiotropic system (Pfeffer et al., 1993). These animals are severely impaired in the clearance of the bacterial pathogen Listeria monocytogenes, die rapidly from infections, and are extraordinarily resistant to lipopolysaccha-

ride-mediated septic shock. Lymphocyte populations, however, are normal and clonal deletion of potentially self-reactive T cells is unimpaired, indicating normal thymocyte development. The creation of p75 TNFR knockout transgenics and, particularly, of double knockouts of p75 and p55 should prove invaluable in dissecting this complex system.

The most recently cloned family member is the Fas ligand, the search for which had approached the status of an immunological Holy Grail (Suda et al., 1993). The reason is that the Fas antigen, broadly expressed on both myeloid and lymphoid cells, including thymocytes, has been characterized as responding to activation (through cross-linking) by inducing apopotic (programmed) cell death. Since this process is fundamental to immune system development and Ca²⁺-independent T cell-mediated cytotoxicity, the ligand may play a crucial role in these phenomena. This is consistent with the finding that a naturally occurring autosomal recessive mutation in mice, lpr (lymphoproliferation), maps to the fas locus, and homozygous animals exhibit lymphadenapathy and autoimmune disease, resembling systemic lupis in humans. One lpr mutant producing a defective Fas protein behaves as a dominant-negative mutation with respect to a phenotypically very similar mutation, gld (generalized lymphoproliferation disease), on a different chromosome, suggesting that fas and gld encode receptor–ligand cognates (Allen et al., 1990). Nagata and colleagues demonstrate that this is indeed the case (Takahashi et al., 1994 [this issue of Cell]). While defects in the Fas system clearly give rise to aberrancies in the immune system, it seems the proximal cause is not thymic failure to eliminate autoreactive clones through apoptosis, as originally suggested (Watanabe-Fukunaga et al., 1992). Indeed, T cell repertoire formation, as well as both positive and negative selection, proceeds normally in homozygous lpr (or gld) animals (Sidman et al., 1992). Instead, Fas appears to be involved in activation-driven T cell suicide, a process by which chronically activated mature T cells undergo apoptosis, suggesting a role for Fas in peripheral tolerance (Russel and Wang, 1993).

The contingent ability to induce death is rather unique to this family and is well established for TNFα, LTα, and FasL. The p55 TNFR and Fas share a 65 residue homology region in the cytoplasmic domains, which deletion studies have established to be crucial for the apoptotic death activity (Takahashi et al., 1994; Tartaglia et al., 1993). However, Fas appears to have a pleiotropic nature, and it is here that Fas mirrors the properties of other family members. Fresh PBT cells, for example, as well as some B cell tumors, respond to Fas activation with proliferation, not death (Mapara et al., 1993; Alderson et al., 1993). Strikingly similar is the behavior of at least three other family members, CD30 and both TNF receptors. In each case, the specific responses, including cell death (apoptotic or necrotic) or proliferation, depend upon cell type, stage of differention, transformation status, and the presence of other stimuli. Thus, elucidation of the full spectrum of FasL activities may prove unexpectedly illuminating. Their fundamental involvement in the immune system and the window they provide on the apoptosis phenomena, crucial to

many aspects of vertebrate development and homeostasis, combine to ensure ever greater interest in this emerging cytokine family.

References

Alderson, M., Armitage, R., Maraskovsky, E., Tough, T., Roux, E., Schooley, K., Ramsdell, F., and Lynch, D. (1993). J. Exp. Med. 178, 2231–2235.

Allen, R., Marshall, J., Roths, R., and Sidman, C. (1990). J. Exp. Med. 172, 1367.

Beers, M., Chaffanet, M., Casalman, H. J., van den Berghe, H., and Maryen, P. (1993). Genomics 16, 214–216.

Banner, D., D'Arcy, A., Janes, W., Gentz, R., Schoenfeld, H.-J., Broger, C., Loetscher, H., and Lesslauer, W. (1993). Cell 73, 431–445.

Beutler, B. (1992). Tumor Necrosis Factors: The Molecules and Their Emerging Role in Medicine (New York: Raven Press).

Browning, J., Ngam-ek, A., Lawton, P., DeMarinis, J., Tizard, R., Chow, E., Hession, C., O'Brine-Greco, B., Foley, S., and Ware, C. (1993). Cell 72, 847–856.

Callard, R., Armitage, R., Fanslow, W., and Spriggs, K. (1993). Immunol. Today 564, 559–564.

de Vos, A., Ultsch, M., and Kossiakoff, A. (1992). Science 255, 306–312.

Eck, M., Ultsch, M., Rinderknecht, E., de Vos, A., and Spring, S. (1992). J. Biol. Chem. 267, 2119–2122.

Farrah, T., and Smith, C. (1992). Nature 358, 26.

Goebel, S., Johnson, G., Perkus, M., Davis, S., Winslow, J., and Paoletti, E. (1990). Virology 179, 247–266.

Goodwin, R., Din, W., Davis-Smith, T., Anderson, D., Gimpel, S., Sato, T., Maliszewski, C., Brannen, C., Copeland, N., Jenkins, N., Farrah, T., Armitage, R., Fanslow, W., and Smith, C. A. (1993). Eur. J. Immunol. 23, 2631–2641.

Jones, E., Stuart, D., and Walker, N. (1989). Nature 338, 225–228.

Mapara, M., Bargou, R., Zugck, C., Doehner, H., Ustaoglu, F., Jonker, R., Krammer, P., and Dorken, B. (1993). Eur. J. Immunol. 23, 702–708.

Pfeffer, K., Matsuyama, T., Kundig, T., Wakeham, A., Kishihara, K., Shahinian, A., Wiegmann, K., Ohashi, P., Kronke, M., and Mak, T. (1993). Cell 73, 457–467.

Russel, J., and Wang, R. (1993). Eur. J. Immunol. 23, 2379–2382.

Schoenfeld, H., Poeschl, B., Frey, J., Loetscher, W., Hunziker, W., Lustig, A., and Zulauf, M. (1990). J. Biol. Chem. 265, 3863–3869.

Shchelkunov, S., Blinov, V., and Sandakhchiev, L. (1993). FEBS Lett. 319, 80–83.

Sidman, C., Marshall, J., and Boehmer, H. (1992). Eur. J. Immunol. 22, 499–504.

Smith, C., Davis, T., Wignall, J., Din, W., Farrah, T., Upton, C., McFadden, G., and Goodwin, R. (1991). Biochem. Biophys. Res. Commun. 176, 335–342.

Smith, C., Gruss, H., Davis, T., Anderson, M. D., Farah, T., Baker, E., Sutherland, R., Brannan, C., Copeland, N., Jenkins, N., Grabstein, K., Gliniac, B., McAllister, L., Fanslow, W., Alderson, M., Falk, B., Gimpel, S., Gillis, S., Din, W., Goodwin, R., and Armitage, R. (1993). Cell 73, 1349–1360.

Suda, T., Takahashi, T., Golstein, P., and Nagata, S. (1993). Cell 75, 1169–1178.

Takahashi, T., Tanaka, M., Brennan, C. I., Jenkins, N. A., Copeland, N. G., Suda, T., and Nagata, S. (1994). Cell 76, this issue.

Tartaglia, L., Ayres, T., Wong, G., and Goeddel, D. (1993). Cell 74, 845–850.

Upton, C., Macen, J., Schreiber, M., and McFadden, G. (1991). Virology 184, 370–382.

Watanabe-Fukunaga, R., Brennan, C., Copeland, N., Jenkins, N., and Nagata, S. (1992). Nature 356, 314–417.